SEQUENCE LISTING

(1) GENERAL INFORMATION:

5   (i) APPLICANT:
          (A) NAME: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL
              RESEARCH ORGANISATION
          (B) STREET: Limestone Avenue
          (C) CITY: Campbell
10   (D) STATE: ACT
          (E) COUNTRY: AUSTRALIA
          (F) POSTAL CODE (ZIP): 2612

          (A) NAME: THE AUSTRALIAN NATIONAL UNIVERSITY
15   (B) STREET: BRIAN LEWIS CRESCENT
          (C) CITY: ACTON
          (D) STATE: ACT
          (E) COUNTRY: AUSTRALIA
          (F) POSTAL CODE (ZIP): 2601
20
          (A) NAME: GOODMAN FIELDER LIMITED
          (B) STREET: LEVEL 42, GROSVENOR PLACE
          (C) CITY: SYDNEY
          (D) STATE: NSW
25   (E) COUNTRY: AUSTRALIA
          (F) POSTAL CODE (ZIP): 2000

          (A) NAME: GROUPE LIMAGRAIN PACIFIC PTY LIMITED
          (B) STREET: LEVEL 31, 1 O'CONNELL STREET
30   (C) CITY: SYDNEY
          (D) STATE: NSW
          (E) COUNTRY: AUSTRALIA
          (F) POSTAL CODE (ZIP): 2000

35   (ii) TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS

       (iii) NUMBER OF SEQUENCES: 17

       (iv) COMPUTER READABLE FORM:
40   (A) MEDIUM TYPE: Floppy disk
          (B) COMPUTER: IBM PC compatible
          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

45   (2) INFORMATION FOR SEQ ID NO: 1:
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 17 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
50   (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: other nucleic acid
              (A) DESCRIPTION: /desc = "pcr primer based on the N-terminal sequence of wSBE I 5' end at
       position 168 of SEQ ID NO:5"
55
          (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

5   (vi) ORIGINAL SOURCE:
            (A) ORGANISM: triticum tauschii
            (F) TISSUE TYPE: Endosperm

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
10

GGCACGCGAG AGACTGG   17

         (2) INFORMATION FOR SEQ ID NO: 2:
            (i) SEQUENCE CHARACTERISTICS:
15   (A) LENGTH: 19 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

20   (ii) MOLECULE TYPE: other nucleic acid
            (A) DESCRIPTION: /desc = "pcr primer in which 5 ' end is at position 1590 of SEQ ID NO:5"

         (iii) HYPOTHETICAL: NO

25   (iv) ANTI-SENSE:

         (v) FRAGMENT TYPE:

         (vi) ORIGINAL SOURCE:
30   (A) ORGANISM: triticum tauschii
            (F) TISSUE TYPE: Endosperm

         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

35   TACATTTCCT TGTCCATCA   19

         (2) INFORMATION FOR SEQ ID NO: 3:
            (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 18 base pairs
40   (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

         (ii) MOLECULE TYPE: other nucleic acid
45   (A) DESCRIPTION: /desc = "pcr primer 5 ' end is at position 1 of SEQ ID NO:5"

         (iii) HYPOTHETICAL: NO

         (iv) ANTI-SENSE:
50
         (v) FRAGMENT TYPE:

         (vi) ORIGINAL SOURCE:
            (A) ORGANISM: triticum tauschii
55   (F) TISSUE TYPE: Endosperm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCACGAGAG CTTGCTCA   18

(2) INFORMATION FOR SEQ ID NO: 4:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "pcr primer 5 ' end is at position 334 of SEQ ID NO:5"

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE:

    (v) FRAGMENT TYPE:

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: triticum tauschii
        (F) TISSUE TYPE: Endosperm

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGTACACAG TTGCGTCATT TTC   23

(2) INFORMATION FOR SEQ ID NO: 5:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2687 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE:

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: triticum tauschii
        (F) TISSUE TYPE: Endosperm

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATCGACGAAG ATGCTCTGCC TCACCGCCCC CTCCTGCTCG CCATCTCTCC CGCCGCGCCC   60

CTCCCGTCCC GCTGCTGACC GGCCCGGACC GGGGATTTCG GCCAAGAGCA AGTTCTCTGT   120

TCCCGTGTCT GCGCCAAGAG ACTACACCAT GGCAACAGCT GAAGATGGTG TTGGCGACCT   180

TCCGATATAC GATCTGGATC CGAAGTTTGC CGGCTTCAAG GAACACTTCA GTTATAGGAT   240

GAAAAAGTAC CTTGACCAGA AACATTCGAT TGAGAAGCAC GAGGGAGGCC TTGAAGAGTT   300

CTCTAAAGGC TATTTGAAGT TTGGGATCAA CACAGAAAAT GACGCAACTG TGTACCGGGA   360

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       ATGGGCCCCT GCAGCAATGG ATGCACAACT TATTGGTGAC TTCAACAACT GGAATGGCTC   420
   5   TGGGCACAGG ATGACAAAGG ATAATTATGG TGTTTGGTCA ATCAGGATTT CCCATGTCAA   480
       TGGGAAACCT GCCATCCCCC ATAATTCCAA GGTTAAATTT CGATTTCACC GTGGAGATGG   540
       ACTATGGGTC GATCGGGTTC CTGCATGGAT TCGTTATGCA ACTTTTGACG CCTCTAAATT   600
  10   TGGAGCTCCA TATGACGGTG TTCACTGGGA TCCACCTTCT GGTGAAAGGT ATGTGTTTAA   660
       GCATCCTCGG CCTCGAAAGC CTGACGCTCC ACGTATTTAC GAGGCTCATG TGGGGATGAG   720
  15   TGGTGAGAGG CCTGAAGTAA GCACATACAG AGAATTTGCA GACAATGTGT TACCGCGCAT   780
       AAAGGCAAAC AACTACAACA CAGTTCAGCT GATGGCAATC ATGGAACATT CCATATTATG   840
       CTTCTTTTGG TACCATGTGA CGAATTTCTT CGCAGTTAGC AGCAGATCAG GAACACCAGA   900
  20   GGACCTCAAA TATCTTGTTG ACAAGGCACA TAGCTTAGGG TTGCGTGTTC TGATGGATGT   960
       TGTCCATAGC CATGCGAGCA GTAATATGAC AGATGGTCTA AATGGCTATG ATGTTGGACA  1020
  25   AAACACACAG GAGTCCTATT CCATACAGG AGAAAGGGGT TATCATAAAC TGTGGGATAG  1080
       TCGCCTGTTC AACTATGCCA ATTGGGAGGT CTTACGGTAT CTTCTTTCTA ATCTGAGATA  1140
       TTGGATGGAC GAATTCATGT TTGACGGCTT CCGATTTGAT GGAGTAACAT CCATGCTATA  1200
  30   TAATCACCAT GGTATCAATA TGTCATTCGC TGGAAATTAC AAGGAATATT TTGGTTTGGA  1260
       TACCGATGTA GATGCAGTTG TTTACATGAT GCTTGCGAAC CATTTAATGC ACAAAATCTT  1320
  35   GCCAGAAGCA ACTGTTGTTG CAGAAGATGT TTCAGGCATG CCAGTGCTTT GTCGGTCAGT  1380
       TGATGAAGGT GGAGTAGGGT TTGACTATCG CCTTGCTATG GCTATTCCTG ATAGATGGAT  1440
       TGACTACTTG AAGAACAAAG ATGACCTTGA ATGGTCAATG AGTGCAATAG CACATACTCT  1500
  40   GACCAACAGG AGATATACGG AAAAGTGCAT TGCATATGCT GAGAGCCACG ATCAGTCTAT  1560
       TGTTGGCGAC AAGACTATGG CATTTCTCTT GATGGACAAG GAAATGTATA CTGGCATGTC  1620
  45   AGACTTGCAG CCTGCTTCAC CTACAATTGA TCGTGGAATT GCACTTCAAA AGATGATTCA  1680
       CTTCATCACC ATGGCCCTTG GAGGTGATGG CTACTTGAAT TTTATGGGTA ATGAGTTTGG  1740
       CCACCCAGAA TGGATTGACT TTCCAAGAGA AGGCAACAAC TGGAGTTATG ATAAATGCAG  1800
  50   ACGCCAGTGG AGCCTCTCAG ACATTGATCA CCTACGATAC AAGTACATGA ACGCATTTGA  1860
       TCAAGCAATG AATGCGCTCG ACGACAAGTT TTCCTTCCTA TCGTCATCAA AGCAGATTGT  1920
  55   CAGCGACATG AATGAGGAAA AGAAGATTAT TGTATTTGAA CGTGGAGATC TGGTCTTCGT  1980
       CTTCAATTTT CATCCCAGTA AAACTTATGA TGGTTACAAA GTCGGATGTG ATTTGCCTGG  2040
       GAAGTACAAG GTAGCTCTGG ACTCCGATGC TCTGATGTTT GGTGGACATG AAGAGTGGC  2100
  60   CCAGTACAAC GATCACTTCA CGTCACCTGA AGGAGTACCA GGAGTACCTG AAACAAACTT  2160
       CAACAACCGC CCTAATTCAT TCAAAGTCCT GTCTCCACCC CGCACTTGTG TGGCTTACTA  2220
  65   TCGCGTCGAG GAAAAAGCGG AAAAGCCTAA GGATGAAGGA CTGCTTCTT GGGGCAAAGC  2280
       TGCTCCTGGG TACATCGATG TTGAAGCCAC TCGTGTCAAA GACGCAGCAG ATGGTGAGGC  2340
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     GACTTCTGGT TCCAAAAAGG CGTCTACAGG AGGTGACTCC AGCAAGAAGG GAATTAACTT 2400

     TGTCTTCGGG TCACCTGACA AAGATAACAA ATAAGCACCA TATCAACGCT TGATCAGAAC 2460

  5  CGTGTACCGA CGTCCTTGTA ATATTCCTGC TATTGCTAGT AGTAGCAATA CTGTCAAACT 2520

     GTGCAGACTT GAGATTCTGG CTTGGACTTT GCTGAGGTTA CCTACTATAT AGAAAGATAA 2580

     ATAAGAGGTG ATGGTGCGGG TCGAGTCCGG CTATATGTGC CAAATATGCG CCATCCCGAG 2640
 10
     TCCTCTGTCA TAAAGGAAGT TTCGGGCTTT CAGCCCAGAA TAAAAAA         2687
```

       (2) INFORMATION FOR SEQ ID NO: 6:
        (i) SEQUENCE CHARACTERISTICS:
 15   (A) LENGTH: 807 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

 20   (ii) MOLECULE TYPE: protein

       (iii) HYPOTHETICAL: NO

       (iv) ANTI-SENSE:
 25
       (vi) ORIGINAL SOURCE:
        (A) ORGANISM: triticum tauschii
        (F) TISSUE TYPE: Endosperm

 30   (ix) FEATURE:
        (A) NAME/KEY: Protein
        (B) LOCATION:1..807
        (D) OTHER INFORMATION:/label= sbeI
          /note= "deduced amino acid sequence from SEQ ID NO:5"
 35
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
```
           Met Leu Cys Leu Thr Ala Pro Ser Cys Ser Pro Ser Leu Pro Pro Arg
           1               5               10              15
 40
           Pro Ser Arg Pro Ala Ala Asp Arg Pro Gly Pro Gly Ile Ser Ala Lys
                       20              25              30

           Ser Lys Phe Ser Val Pro Val Ser Ala Pro Arg Asp Tyr Thr Met Ala
 45                    35              40              45

           Thr Ala Glu Asp Gly Val Gly Asp Leu Pro Ile Tyr Asp Leu Asp Pro
                   50              55              60

 50        Lys Phe Ala Gly Phe Lys Glu His Phe Ser Tyr Arg Met Lys Lys Tyr
           65              70              75              80

           Leu Asp Gln Lys His Ser Ile Glu Lys His Glu Gly Gly Leu Glu Glu
 55                        85              90              95

           Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Glu Asn Asp Ala
                       100             105             110

           Thr Val Tyr Arg Glu Trp Ala Pro Ala Ala Met Asp Ala Gln Leu Ile
 60                    115             120             125
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        Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His Arg Met Thr Lys Asp
            130                 135                 140

  5     Asn Tyr Gly Val Trp Ser Ile Arg Ile Ser His Val Asn Gly Lys Pro
            145                 150                 155                 160

        Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe His Arg Gly Asp
                            165                 170                 175

 10     Gly Leu Trp Val Asp Arg Val Pro Ala Trp Ile Arg Tyr Ala Thr Phe
                        180                 185                 190

        Asp Ala Ser Lys Phe Gly Ala Pro Tyr Asp Gly Val His Trp Asp Pro
                        195                 200                 205

 15     Pro Ser Gly Glu Arg Tyr Val Phe Lys His Pro Arg Pro Arg Lys Pro
                210                 215                 220

 20     Asp Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser Gly Glu Arg
            225                 230                 235                 240

        Pro Glu Val Ser Thr Tyr Arg Glu Phe Ala Asp Asn Val Leu Pro Arg
                            245                 250                 255

 25     Ile Lys Ala Asn Asn Tyr Asn Thr Val Gln Leu Met Ala Ile Met Glu
                        260                 265                 270

        His Ser Ile Leu Cys Phe Phe Trp Tyr His Val Thr Asn Phe Phe Ala
                    275                 280                 285

 30     Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr Leu Val Asp
            290                 295                 300

 35     Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val Val His Ser
            305                 310                 315                 320

        His Ala Ser Ser Asn Met Thr Asp Gly Leu Asn Gly Tyr Asp Val Gly
                        325                 330                 335

 40     Gln Asn Thr Gln Glu Ser Tyr Phe His Thr Gly Glu Arg Gly Tyr His
                        340                 345                 350

        Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn Trp Glu Val Leu
                355                 360                 365

 45     Arg Tyr Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp Glu Phe Met Phe
            370                 375                 380

 50     Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr Asn His His
            385                 390                 395                 400

        Gly Ile Asn Met Ser Phe Ala Gly Asn Tyr Lys Glu Tyr Phe Gly Leu
                        405                 410                 415

 55     Asp Thr Asp Val Asp Ala Val Val Tyr Met Met Leu Ala Asn His Leu
                    420                 425                 430

        Met His Lys Ile Leu Pro Glu Ala Thr Val Val Ala Glu Asp Val Ser
                435                 440                 445

 60     Gly Met Pro Val Leu Cys Arg Ser Val Asp Glu Gly Gly Val Gly Phe
            450                 455                 460
```

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        Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Arg Trp Ile Asp Tyr Leu
        465             470             475             480

   5    Lys Asn Lys Asp Asp Leu Glu Trp Ser Met Ser Ala Ile Ala His Thr
                        485             490             495

        Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile Ala Tyr Ala Glu Ser
                    500             505             510

  10    His Asp Gln Ser Ile Val Gly Asp Lys Thr Met Ala Phe Leu Leu Met
                    515             520             525

        Asp Lys Glu Met Tyr Thr Gly Met Ser Asp Leu Gln Pro Ala Ser Pro
                530             535             540

  15    Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile His Phe Ile Thr
        545             550             555             560

        Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe
  20                    565             570             575

        Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn Asn Trp Ser
                    580             585             590

  25    Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Ser Asp Ile Asp His Leu
                    595             600             605

        Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met Asn Ala Leu Asp
            610             615             620

  30    Asp Lys Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile Val Ser Asp Met
        625             630             635             640

        Asn Glu Glu Lys Lys Ile Ile Val Phe Glu Arg Gly Asp Leu Val Phe
  35                    645             650             655

        Val Phe Asn Phe His Pro Ser Lys Thr Tyr Asp Gly Tyr Lys Val Gly
                    660             665             670

  40    Cys Asp Leu Pro Gly Lys Tyr Lys Val Ala Leu Asp Ser Asp Ala Leu
                    675             680             685

        Met Phe Gly Gly His Gly Arg Val Ala Gln Tyr Asn Asp His Phe Thr
            690             695             700

  45    Ser Pro Glu Gly Val Pro Gly Val Pro Glu Thr Asn Phe Asn Asn Arg
        705             710             715             720

        Pro Asn Ser Phe Lys Val Leu Ser Pro Pro Arg Thr Cys Val Ala Tyr
  50                    725             730             735

        Tyr Arg Val Glu Glu Lys Ala Glu Lys Pro Lys Asp Glu Gly Ala Ala
                740             745             750

  55    Ser Trp Gly Lys Ala Ala Pro Gly Tyr Ile Asp Val Glu Ala Thr Arg
                755             760             765

        Val Lys Asp Ala Ala Asp Gly Glu Ala Thr Ser Gly Ser Lys Lys Ala
            770             775             780

  60    Ser Thr Gly Gly Asp Ser Ser Lys Lys Gly Ile Asn Phe Val Phe Gly
        785             790             795             800
```

Ser Pro Asp Lys Asp Asn Lys
                    805

    (2) INFORMATION FOR SEQ ID NO: 7:
     (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 319 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE:

    (vi) ORIGINAL SOURCE:
     (A) ORGANISM: triticum tauschii
     (F) TISSUE TYPE: Endosperm

    (ix) FEATURE:
     (A) NAME/KEY: misc_signal
     (B) LOCATION:1..319
     (D) OTHER INFORMATION:/function= "3' untranslated region
     of wSBE I-D4 cDNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
GCGACTTCTG GTTCCAAAAA GGCGTCTACA GGAGGTGACT CCAGCAAGAA GGGAATTAAC   60

TTTGTCTTCG GGTCACCTGA CAAAGATAAC AAATAAGCAC CATATCAACG CTTGATCAGA  120

ACCGTGTACC GACGTCCTTG TAATATTCCT GCTATTGCTA GTAGTAGCAA TACTGTCAAA  180

CTGTGCAGAC TTGAGATTCT GGCTTGGACT TTGCTGAGGT TACCTACTAT ATAGAAAGAT  240

AAATAAGAGG TGATGGTGCG GGTCGAGTCC GGCTATATGT GCCAAATATG CGCCATCCCG  300

AGTCCTCTGT CATAAAGGA              319
```

    (2) INFORMATION FOR SEQ ID NO: 8:
     (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 4890 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE:

    (vi) ORIGINAL SOURCE:
     (A) ORGANISM: triticum tauschii
     (F) TISSUE TYPE: Endosperm

    (ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION:1..4890
(D) OTHER INFORMATION:/function= "promoter containing
  sequence of SBE I"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
GGGTGGCGGG TCGGGCGGCA AGGCGCGGGG CGGCGGGGCG GCCGGGGCGG CGCGGCGGCG    60
CGGGCGGCAG CGGCGGCTAG GGTTTCGCGG CGGCGGCGAC TTGGGCTGAG GCGGGGCACG   120
GGCTGCGGCT TTAAAGGCCG GCCAGGCTGA GGTGTCCGGG TCGGACACGG CCCGTAAGGC   180
GGTTGACTTT AAAAAATAAT AATTCGGACA TGCAAAAAAG TAAGAAAAGA AATAATAAAC   240
GGACTCCAAA AATCCCGAAG TAAATTTTTC CCCATTCTTA AAAATAAGCC GGACAAGATG   300
AACATTTATT TGGGCCTAAA ATGCAATTTT GAAAAATGCG TATTTTTCCT AATTCGGAAT   360
AAAATCAAAT AAAATCCAAA TAAAATCAAA TATTTGTTTT TAATATTTTT CCTCCAATAT   420
TTCATTATTT GTGAAGAAGT CATTTTATCC CATCTCATAT ATTTTGATAT GAAATATTTT   480
CGGAGAGAAA AATAATTAAA ACAAATGATC CTATTTTCAA AATTTGAGAA AACCCAAATA   540
TGAAAATAAC GAAATCCCCA ACTCTCTCCG TGGGTCCTTG AGTTGCGTGA AATTTCTAGG   600
ATCACAAATC AAAATGCAAT AAAATATGAT ATGCATGATG ATCTAATGTA TAACATTCCA   660
ATTGAAAATT TGGGATGTTA CATATAACTC AAATTCTATA ATTATGAACA CAGAAATATT   720
AATGTAGAAC TCTATTTTGT TTTGAAATTG TATTATTTTT TAGAATTAGT CTAGAGCATT   780
TCGTGAACTT GAATCAAACC TTTAAATAAA ACAAAGCATA AAAATGACAA ATTCACATAT   840
GAAATAACTT GTGTTACATA GATTTATTAC AATAGCGTTG TATGTGTGTA TGTGTGCGTG   900
AGTGCCTATG GTAATATCAA TAAATATCTT GATAGATGTT CTACAATTC ACGGGTCTAA    960
CTAGTAATGC AATGCAATGC ATGCTAAAAG AATAGAACCT TAGTTTCATT TAACTAACAA  1020
TTTTCAAATG TATGAGTTGC CAACAAGTGG CATACTTGGC ACTGTTTGTT TGTTCATTTT  1080
ATGGAAAGTT CTTCTCTTTT TACATGGTTT AGATTCCAGC ATGTAGCCAC AAAATATGAT  1140
TGTCAAAAGA TAATACCTCA TAATACAATT CCACTAAAGT CACCTAGCCC AAGTGACCGA  1200
CCTGATCCTG AAATAAAATC AGAAGATTTG GTGTCATCAT CATGACAACA AATTATTAGG  1260
CGGTAGATCT TGTGGTAGTA CTCATGATGT AAAATTATCA AGAGGGAGAG AATGTATGGA  1320
GATTTATGTG AAGTACATCG TACACCAGAC ATAGTTGACA CATCGATTTT TTAAGATACA  1380
TTTGGACGCG CCTTGTGGGA GTGTAAAGTA CTACCATGTA TTAGAAGAGG TGAAATGAGA  1440
AATGCCATAG CTAGCAAGTA GGCCTAGTTA AGGAAATTCT TCCTTAGATC CCCTTCTCCC  1500
GAAGAGTGAA GTGCTTCAAC TAAAGGTTAG ACCCACTTAA AAAATGTCAC TTTGAATCTT  1560
TGCTTCCCTT GTCGTAATCC TGTGCATTTG TAGGTCCCTC GGATCTGAGC CCTTTCTCCA  1620
AGCCCTTCAT TGGATTCCCC TGGATGTCTT TTTGTTACAT TTTATTGAAG TGAGAGTGAA  1680
TTATTATATG CCCATAGGAG GTGGGATATA AAGGCTGTTG GTATTCTGCA CCATACATGC  1740
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TAGAGTAGGG AGGAGAGGCT GGTGCATGAT ACATGGTGGA CTAGCCCATA TATTTACCCC 1800

TCCCCCACCC ACTAACAAGT TTTTTTTATT AGGTCTTCAT CCTCTGATTT GTTTTTCTGT 1860

TAGCCCATTC TTCATCATGG ACTTATTAAT CATGATTAGT TTCTTGGATT TTTGTTTACT 1920

TGACTTGAAT TTGACAATGT GCCTCATATA TGGCATGTGG GACTGATAGG AAGATATATT 1980

CTCACAACAT TAACTTAAAA AGGATTATTT TTTTGGTGCA GTCGTAAAGA AAACTACTTT 2040

CTTTTATGCT AAAAGTTATT CAAACATAGA TTTATAAACA AAGGATATCA CCATGCATGA 2100

CCATGCGCTC TCTCATGTTT ACTCTAGAAA CCATATATCT CTTTGTTGCA AAATATTTAA 2160

TCTATCCTCC TTGTTTCTGG GAATGAGTCG GGGAAGGTAA TCTTAGGGAA GGTTAAAGTG 2220

AGGCAAGTAA GAGCAACTCT AGCAGAGTCG CGATATGCCC AATCGCCATA ATGCCAATAT 2280

GGCATTTTTG GCCCAAAATG GCACTTCAGA AGAGTCACCA TATCCCTTCG GATAGCCATA 2340

ATTTAGGGAG CTCGCTCCAC AAACAAGCTT CGAGCCTCCA AATATGGAGG CCATGGATTC 2400

GTTGTTTGGC ACTCACTCCA TATCCAACCG CAAGCGCATG CATGAGGGAA GTTTTAGCTT 2460

CTTCCTCCTT GCGCCAACGC CGGGATTTTA CACAGCGCAT TACAGGTACA TGAACCAGCA 2520

TGCACAGATA ATCACCGACG AGTGGGGTGA CAAGAAGGAT AAGCACCCTC CCATTAGTGG 2580

TGCGCCCACT CCCCTCAAAT TCATGAGGCA GCCATTTGGA TGGTCATCGC GTGGCATAAG 2640

CTCCGACTAT AAAATCTCAA CGGCATCACC AAAACCATAG CTGCCGCCTC CCCCTTCCTC 2700

GGCATCACCT CCCCAAGACA TCTCCTCCCC TCTATGCCAC AATGTCATCA TTATGGAGAG 2760

ACACAACTAC TGGTAAACCG CATACCCAAT CATGGTTTAC CGGCAGTGCG AACCCCACCT 2820

TCCTCCCACG ATGGTAGGAT ATTCTCCTCC TAGAATGGCG CGTGTGGCGC TTCCTCCTCC 2880

CGAGGCTGAT ATGTCGGCTC CCATGATGGC GTGCATCATT GATTTGGCGC TTCGGGTCCA 2940

TCATACATGT TAACGAGGTC ATCCCCATTG ATGTCGTTGG TCCCCTTGCC CCCCAGTCGG 3000

ATCCTGAGGA CCCGTTCGAT GTCGCAATGC GACTCTCCAA ACTCAAAGCT CACAATGAGG 3060

AGTACGTCCT CTAGGAGTTC CGCCCCGCAA CCATCTATAA GGAGGAGCAA CGATAGCTCT 3120

CCCCTACGCC TTCCTCGACG ATCTCTCTTA GGAGGACAAC GGCTAGACGA CGGCGGCGGC 3180

GGCGAAGGTA CTGCAGGTAG TAGAACATAG CAATGTCGAA TGGCGACATT GCATATTTTG 3240

AAAATGTCGC TCAACGACTT TTGAAGTCGC AAATAAAATG TAGTGTGACT ACTTTTGGCC 3300

AGCAATATAA GTTTATCACA TTTGATAATG ATTTGAACCG GTGTGGTTCA ACTAAATGTA 3360

CCATAAATTG AACATACAAA TTTTTAGCAA ATGAAAAAG AAACAAGTAA GACCACAAAT 3420

ATGAAAGCCG CATATCGCGA CTATGTGTTT GAGCCGCAGC TGCCAAGTAC ATATGAAGCG 3480

TACTCCATAT GACATACGAC AACCATACAT ATGAAGACTC TACTAGAGTT CTCTAAGGCC 3540

GCTTTTAGCG CCTTTCGTGC AGTGGTGCCC ATAGGGAGTG AGGGTAGTTG GACTGTTCGT 3600

TTCCCCTTTT TTCATTTCTT TGAAATCTAT TTTATTTTTT TTCTCTTTTG TAGGTTTCCC 3660

AAATTTATAT ACCATTTTTC TGTTTCTCGC TATTTTTTGT TGTTATATTC TAGTTTCATA 3720

TTTTTCTATT ATTAATTTGT GTCTCTTATG AGAAGTCCAG ACTTGCATAT GGAGGTGCAC 3780
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ACACAAACAT ATAAAGTATA AATACTAACT TGAGAAGTAT GTTTGCGTGG TCAAAAAAAC 3840

ATCATCAAAA CCTGCCAATA TGAGATATAG TTTTGAATAT ATCAATATGA GCAACGCAAC 3900

CATTTAAAAT GTGAACAATT GTTTTTTTAG AAAAAATATA AGAAATAACT CCAACCCAGC 3960

CAAACCACAT GCTATACACT TGCTCCATAT GAAACCATGT TTGCTATTGG GCAGTTGCCT 4020

GAAACCGAAA GTAATGTTAG CCGTTTTTCT ATTCAAAGAA GAAGGAGAGT CGAGGTGACG 4080

CGATGCTTAG ACGTGAGATG GGGATGACCA CAACGTCCCT ACAGAGACCT CACCGGAGAT 4140

GGGGACATTG CAGTTGACAC GAGAGCGGTG AGGGGCTGCG ATGCGTGTGC GGCAACATGT 4200

GGCGAGGCGG ACGTCGGGCT GGCAGGTAGG GGGGAGGGGG AAGGACCGGG GGAGGAAGAA 4260

GAGGAGTAGC CTGCAAAACA TGGTACACCA GTTTTCTGCC CTACGAAAAC CTCATTTCAT 4320

TCCCCCACCC TGACAAGCAA CAACCAACCA TCGCAGTCCC ACATGTCCCT CTGGTCTTTG 4380

CAAAAAGTAA TTGTTCTTGC TGGACAGCGC AAAGAGTAAA CTTTTGTTAG TTTTCATTTC 4440

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GGCCCAGCGG CGCACGACCG TCCACGTGCA CCCCGGCCCT CCCGGGCCCG CAGATCCGTT 4680

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TTCCTGTCCA AAGCGGCCAC GGACCGGAAA AAAATCACGC CTTTCCGTTG GGTCTCCGGC 4800

GCCACACTCC TCCTCCGGCC GATATAAAGC GCGCGGGGCC ACGGGCCCGG CGCAAAATGG 4860

GATTCCCGTC CGCCGCCATG GAGGAAGATG                4890
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(2) INFORMATION FOR SEQ ID NO: 9:
  (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 6228 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE:

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: triticum tauschii
  (F) TISSUE TYPE: Endosperm

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION: 1
  (D) OTHER INFORMATION:/product= "coding region of wSBE I-D4 gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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(2) INFORMATION FOR SEQ ID NO: 10:
   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 11463 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE:

   (vi) ORIGINAL SOURCE:
   (A) ORGANISM: triticum tauschii
   (F) TISSUE TYPE: Endosperm

   (ix) FEATURE:
   (A) NAME/KEY: misc_feature
   (B) LOCATION:1..11463
   (D) OTHER INFORMATION:/product= "complete sequence of the
   starch branching enzyme II gene"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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      AGGCGCATTC GAACTGGACA GACGCTCACG CAGGAGCCCA GCACCACAGG CTTGAGCCTG  240

      ACAGCGGACG TGAGTGCGTG ACACATGGGG TCATCTATGG GCGTCGGAGC AAGGAAGAGA  300

      GACGCACATG AACACCATGA TGATGCTATC AGGCCTGATG GAGGGAGCAA CCATGCACCT  360

      TTTCCCCTCT GGAAATTCAT AGCTCACACT TTTTTTTAAT GGAAGCAAGA GTTGGCAAAC  420

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        CACGTTGCTC CCCCTTCTCA TCGCTTCTCA ATTAATATCT CCATCACTCG GGTTCCGCGC 1140
10      TGCATTTCGG CCGGCGGGTT GAGTGAGATC TGGGCGACTG GCTGACTCAA TCACTACGCG 1200
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TTGGCTAACT GTTCCTGTTA ATCTGTTCTT ACACATGTTG ATATTCTATT CTTATGCAGG 6420

TATTGAGATT CTTACTGTCA AACGCGAGAT GGTGGCTTGA AGAATATAAG TTTGATGGAT 6480

TTCGATTTGA TGGGGTGACC TCCATGATGT ATACTCACCA TGGATTACAA GTAAGTCATC 6540

AAGTGGTTTC AGTAACTTTT TTAGGGCACT GAAACAATTG CTATGCATCA TAACATGTAT 6600

CATGATCAGG ACTTGTGCTA CGGAGTCTTA GATAGTTCCC TAGTATGCTT GTACAATTTT 6660

ACCTGATGAG ATCATGGAAG ATTGGAAGTG ATTATTATTT ATTTTCTTTC TAAGTTTGTT 6720

TCTTGTTCTA GATGACATTT ACTGGGAACT ATGGCGAATA TTTTGGATTT GCTACTGATG 6780

TTGATGCGGT AGTTTACTTG ATGCTGGTCA ACGATCTAAT TCATGGACTT TATCCTGATG 6840

CTGTATCCAT TGGTGAAGAT GTAAGTGCTT ACAGTATTTA TGATTTTTAA CTAGTTAAGT 6900

AGTTTTATTT TGGGGATCAG TCTGTTACAC TTTTTGTTAG GGGTAAAATC TCTCTTTTCA 6960
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       TAACAATGCT AATTTATACC TTGTATGATA ATGCATCACT TAGTAATTTG AAAAGTGCAA 7020

   5   GGGCATTCAA GCTTACGAGC ATATTTTTTG ATGGCTGTAA TTTATTTGAT AGTATGCTTG 7080

       TTTGGGTTTT TCAATAAGTG GGAGTGTGTG ACTAATGTTG TATTATTTAT TTAATTGCGG 7140

       AAGAAATGGG CAACCTTGTC AATTGCTTCA GAAGGCTAAC TTTGATTCCA TAAACGCTTT 7200

  10   GGAAATGAGA GGCTATTCCC AAGGACATGA ATTATACTTC AGTGTGTTCT GTACATGTAT 7260

       TTGTAATAGT GGTTTAACTT AAATTCCTGC ACTGCTATGG AATCTCACTG TATGTTGTAG 7320

       TGTACACATC CACAAACAAG TAATCCTGAG CTTTCAACTC ATGAGAAAAT AGAGTCCGCT 7380

  15   TCTGCCAGCA TTAACTGTTC ACAGTTCTAA TTTGTGTAAC TGTGAAATTG TTCAGGTCAG 7440

       TGGAATGCCT ACATTTTGCA TCCCTGTTCC AGATGGTGGT GTTGGTTTTG ACTACCGCCT 7500

  20   GCATATGGCT GTAGCAGATA AATGGATTGA ACTCCTCAAG TAAGTGCAGG AATATTGGTG 7560

       ATTACATGCG CACAATGATC TAGATTACAT TTTCTAAATG GTAAAAAGGA AAATATGTAT 7620

  25   GTGAATATCT AGACATTTGC CTGTTATCAG CTTGAATACG AGAAGTCAAA TACATGATTT 7680

       AAATAGCAAA TCTCGGAAAT GTAATGGCTA GTGTCTTTAT GCTGGGCAGT GTACATTGCG 7740

       CTGTAGCAGG CCAGTCAACA CAGTTAGCAA TATTTTCAGA AACAATATTA TTTATATCCG 7800

  30   TATATGAGAA AGTTAGTATA TAAACTGTGG TCATTAATTG TGTTCACCTT TTGTCCTGTT 7860

       TAAGGATGGG CAGTAGGTAA TAAATTTAGC CAGATAAAAT AAATCGTTAT TAGGTTTACA 7920

  35   AAAGGAATAT ACAGGGTCAT GTAGCATATC TAGTTGTAAT TAATGAAAAG CTGACAAAA 7980

       GGCTCGGTAA AAAAAACTTT ATGATGATCC AGATAGATAT GCAGGAACGC GACTAAAGCT 8040

       CAAATACTTA TTGCTACTAC ACAGCTGCCA ATCTGTCATG ATCTGTGTTC TGCTTTGTGC 8100

  40   TATTTAGATT TAAATACTAA CTCGATACAT TGGCAATAAT AAACTTAACT ATTCAACCAA 8160

       TTTGGTGGAT ACCAGAATTT CTGCCCTCTT GTTAGTAATG ATGTGCTCCC TGCTGCTGTT 8220

  45   CTCTGCCGTT ACAAAAGCTG TTTTCAGTTT TTTGCATCAT TATTTTTGTG TGTGAGTAGT 8280

       TTAAGCATGT TTTTTGAAGC TGTGAGCTGT TGGTACTTAA TACATTCTTG GAAGTGTCCA 8340

       AATATGCTGC AGTGTAATTT AGCATTTCTT TAACACAGGC AAAGTGACGA ATCTTGGAAA 8400

  50   ATGGGCGATA TTGTGCACAC CCTAACAAAT AGAAGGTGGC TTGAGAAGTG TGTAACTTAT 8460

       GCAGAAAGTC ATGATCAAGC ACTAGTTGGT GACAAGACTA TTGCATTCTG GTTGATGGAT 8520

  55   AAGGTACTAG CTGTTACTTT TGGACAAAAG AATTACTCCC TCCCGTTCCT AAATATAAGT 8580

       CTTTGTAGAG ATTCCACTAT GGACCACATA GTATATAGAT GCATTTTAGA GTGTAGATTC 8640

       ACTCATTTTG CTTCGTATGT AGTCCATAGT GAAATCTCTA CAGAGACTTA TATTTAGGAA 8700

  60   CGGAGGGAGT ACATAATTGA TTTGTCTCAT CAGATTGCTA GTGTTTTCTT GTGATAAAGA 8760

       TTGGCTGCCT CACCCATCAC CAGCTATTTC CCAACTGTTA CTTGAGCAGA ATTTGCTGAA 8820

  65   AACGTACCAT GTGGTACTGT GGCGGCTTGT GAACTTTGAC AGTTATGTTG CAATTTTCTG 8880

       TTCTTATTTA TTTGATTGCT TATGTTACCG TTCATTTGCT CATTCCTTTC CGAGACCAGC 8940
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CAAAGTCACG TGTTAGCTGT GTGATCTGTT ATCTGAATCT TGAGCAAATT TTATTAATAG 9000

GCTAAAATCC AACGAATTAT TTGCTTGAAT TTAAATATAC AGACGTATAG TCACCTGGCT 9060

CTTTCTTAGA TGATTACCAT AGTGCCTGAA GGCTGAAATA GTTTTGGTGT TTCTTGGATG 9120

CCGCCTAAAG GAGTGATTTT TATTGGATAG ATTCCTGGCC GAGTCTTCGT TACAACATAA 9180

CATTTTGGAG ATATGCTTAG TAACAGCTCT GGGAAGTTTG GTCACAAGTC TGCATCTACA 9240

CGCTCCTTGA GGTTTTATTA TGGCGCCATC TTTGTAACTA GTGGCACCTG TAAGGAAACA 9300

CATTCAAAAG GAAACGGTCA CATCATTCTA ATCAGGACCA CCATACTAAG AGCAAGATTC 9360

TGTTCCAATT TTATGAGTTT TTGGGACTCC AAAGGGAACA AAAGTGTCTC ATATTGTGCT 9420

TATAACTACA GTTGTTTTTA TACCAGTGTA GTTTTATTCC AGGACAGTTG ATACTTGGTA 9480

CTGTGCTGTA AATTATTTAT CCGACATAGA ACAGCATGAA CATATCAAGC TCTCTTTGTG 9540

CAGGATATGT ATGATTTCAT GGCTCTGGAT AGGCTTCAAC TCTTCGCATT GATCGTGGCA 9600

TAGCATTACA TAAAATGATC AGGCTTGTCA CCATGGGTTT AGGTGGTGAA GGCTATCTTA 9660

ACTTCATGGG AAATGAGTTT GGGCATCCTG GTCAGTCTTT ACAACATTAT TGCATTCTGC 9720

ATGATTGTGA TTTACTGTAA TTTGAACCAT GCTTTTCTTT CACATTGTAT GTATTATGTA 9780

ATCTGTTGCT TCCAAGGAGG AAGTTAACTT CTATTTACTT GGCAGAATGG ATAGATTTTC 9840

CAAGAGGCCC ACAAACTCTT CCAACCGGCA AAGTTCTCCC CTGGAAATAA CAATAGTTAT 9900

GATAAATGCC GCCGTAGATT TGATCTTGTA AGTTTTAGCT GTGCTATTAC ATTCCCTCAC 9960

TAGATCTTTA TTGGCCATTT ATTTCTTGAT GAAATCATAA TGTTTGTTAG GAAAGATCAA 10020

CATTGCTTTT GTAGTTTTGT AGACGTTAAC ATAAGTATGT GTTGAGAGTT GTTGATCATT 10080

AAAAATATCA TGATTTTTTG CAGGGAGATG CAGATTTTCT TAGATATCGT GGTATGCAAG 10140

AGTTCGATCA GGCAATGCAG CATCTTGAGG AAAAATATGG GGTATGTCAC TGGTTTGTCT 10200

TTGTTGCATA ACAAGTCACA GTTTAACGTC AGTCTCTTCA AGTGGTAAAA AAAGTGTAGA 10260

ATTAATTCCT GTAATGAGAT GAAAACTGTG CAAAGGCGGA GCTGGAATTG CTTTTCACCA 10320

AAACTATTTT CTTAAGTGCT TGTGTATTGA TACATATACC AGCACTGACA ATGTAACTGC 10380

AGTTTATGAC ATCTGAGCAC CAGTATGTTT CACGGAAACA TGAGGAAGAT AAGGTGATCA 10440

TCCTCAAAAG AGGAGATTTG GTATTGTTT TCAACTTCCA CTGGAGCAAT AGCTTTTTTG 10500

ACTACCGTGT TGGGTGTTCC AAGCCTGGGA AGTACAAGGT ATGCTTGCCT TTTCATTGTC 10560

CACCCTTCAC CAGTAGGGTT AGTGGGGGCT TCTACAACTT TTAATTCCAC ATGGATAGAG 10620

TTTGTTGGTC GTGCAGCTAT CAATATAAAG AATAGGGTAA TTTGTAAAGA AAAGAATTTG 10680

CTCGAGCTGT TGTAGCCATA GGAAGGTTGT TCTTAACAGC CCCGAAGCAC ATACCATTCA 10740

TTCATATTAT CTACTTAAGT GTTTGTTTCA ATCTTTATGC TCAGTTGGAC TCGGTCTAAT 10800

ACTAGAACTA TTTTCCGAAT CTACCCTAAC CATCCTAGCA GTTTTAGAGC AGCCCATTT 10860

GGACAATTGG CTGGGTTTTT GTTAGTTGTG ACAGTTTCTG CTATTTCTTA ATCAGGTGGC 10920

CTTGGACTCT GACGATGCAC TCTTTGGTGG ATTCAGCAGG CTTGATCATG ATGTCGACTA 10980
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CTTCACAACC GTAAGTCTGG GCTCAAGCGT CACTTGACTC GTCTTGACTC AACTGCTTAC 11040

AAATCTGAAT CAACTTCCCA ATTGCTGATG CCCTTGCAGG AACATCCGCA TGACAACAGG 11100

CCGCGCTCTT TCTCGGTGTA CACTCCGAGC AGAACTGCGG TCGTGTATGC CCTTACAGAG 11160

TAAGAACCAG CAGCGGCTTG TTACAAGGCA AAGAGAGAAC TCCAGAGAGC TCGTGGATCG 11220

TGAGCGAAGC GACGGGCAAC GGCGCGAGGC TGCTCCAAGC GCCATGACTG GGAGGGGATC 11280

GTGCCTCTTC CCCAGATGCC AGGAGGAGCA GATGGATAGG TAGCTTGTTG GTGAGCGCTC 11340

GAAAGAAAAT GGACGGGCCT GGGTGTTTGT TGTGCTGCAC TGAACCCTCC TCCTATCTTG 11400

CACATTCCCG GTTGTTTTTG TACATATAAC TAATAATTGC CCGTGCGCTC AACGTGAAAA 11460

TCC                    11463
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(2) INFORMATION FOR SEQ ID NO: 11:
   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 2662 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE:

   (vi) ORIGINAL SOURCE:
   (A) ORGANISM: triticum tauschii
   (F) TISSUE TYPE: Endosperm

   (ix) FEATURE:
   (A) NAME/KEY: misc_feature
   (B) LOCATION:1..2651
   (D) OTHER INFORMATION:/product= "nucleotide sequence of
   cDNA wheat SSS I"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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TCTCCCACTC TTCTCTCCCC GCGCACACCG AGTCGGCACC GGCTCATCAC CCATCACCTC 60

GGCCTCGGCC ACCGGCAAAC CCCCCGATCC GCTTTTGCAG GCAGCGCACT AAAACCCCGG 120

GGAGCGCGCC CCGCGGCAGC AGCAGCACCG CAGTGGGAGA GAGAGGCTTC GCCCCGGCCC 180

GCACCGAGCG GGGCGATCCA CCGTCCGTGC GTCCGCACCT CCTCCGCCTC CTCCCCTGTC 240

CCGCGCGCCC ACACCCATGG CGGCGACGGG CGTCGGCGCC GGGTGCCTCG CCCCCAGCGT 300

CCGCCTGCGC GCCGATCCGG CGACGGCGGC CCGGGCGTCC GCCTGCGTCG TCCGCGCGCG 360

GCTCCGGCGC TTGGCGCGGG GCCGCTACGT TGCCGAGCTC AGCAGGGAGG GCCCCGCGGC 420

GCGCCCCGCG CAGCAGCAGC AACTGGCCCC GCCGCTCGTG CCAGGCTTCC TCGCGCCGCC 480

GCCGCCCGCG CCCGCCCAGT CGCCGGCCCC GACGCAGCCG CCCCTGCCGG ACGCCGGCGT 540

GGGGGAACTC GCGCCCGACC TCCTGCTCGA AGGGATTGCT GAGGATTCCA TCGACAGCAT 600
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      AATTGTGGCT GCAAGTGAGC AGGATTCTGA GATCATGGAT GCGAATGAGC AACCTCAAGC  650
  5   TAAAGTTACA CGTAGCATCG TGTTTGTGAC TGGTGAAGCT GCTCCTTATG CAAAGTCAGG  720
      GGGGCTGGGA GATGTTTGTG GTTCGTTACC AATTGCTCTT GCTGCTCGTG GTCACCGTGT  730
      GATGGTTGTA ATGCCAAGAT ACTTGAATGG GTCCTCTGAT AAAAACTATG CAAAGGCATT  840
 10   ATACACTGGG AAGCACATTA AGATTCCATG CTTTGGGGGA TCACATGAAG TGACCTTTTT  900
      TCATGAGTAT AGAGACAACG TCGATTGGGT GTTTGTCGAT CATCCGTCAT ATCATAGACC  960
 15   AGGAAGTTTA TATGGAGATA ATTTTGGTGC TTTTGGTGAT AATCAGTTCA GATACACACT 1020
      CCTTTGCTAT GCTGCATGCG AGGCCCCACT AATCCTTGAA TTGGGAGGAT ATATTTATGG 1080
      ACAGAATTGC ATGTTTGTTG TGAACGATTG GCATGCCAGC CTTGTGCCAG TCCTTCTTGC 1140
 20   TGCAAAATAT AGACCATACG GTGTTTACAG AGATTCCCGC AGCACCCTTG TTATACATAA 1200
      TTTAGCACAT CAGGGTCTGG AGCCTGCAAG TACATATCCT GATCTGGGAT GCCACCTGA 1260
 25   ATGGTATGGA GCTTTAGAAT GGGTATTTCC AGAATGGGCA AGGAGGCATG CCCTTGACAA 1320
      GGGTGAGGCA GTTAACTTTT TGAAAGGAGC AGTCGTGACA GCAGATCGAA TTGTGACCGT 1380
      CAGTCAGGGT TATTCATGGG AGGTCACAAC TGCTGAAGGT GGACAGGGCC TCAATGAGCT 1440
 30   CTTAAGCTCC CGAAAAAGTG TATTGAATGG AATTGTAAAT GGAATTGACA TTAATGATTG 1500
      GAACCCCACC ACAGACAAGT GTCTCCCTCA TCATTATTCT GTCGATGACC TCTCTGGAAA 1560
 35   GGCCAAATGT AAAGCTGAAT TGCAGAAGGA GCTGGGTTTA CCTGTAAGGG AGGATGTTCC 1620
      TCTGATTGGC TTTATTGGAA GACTGGATTA CCAGAAAGGC ATTGATCTCA TTAAAATGGC 1680
      CATTCCAGAG CTCATGAGGG AGGACGTGCA GTTTGTCATG CTTGGATCTG GGATCCAAT 1740
 40   TTTTGAAGGC TGGATGAGAT CTACCGAGTC GAGTTACAAG GATAAATTCC GTGGATGGGT 1800
      TGGATTTAGT GTTCCAGTTT CCCACAGAAT AACTGCAGGT TGCGATATAT TGTTAATGCC 1860
 45   ATCCAGGTTT GAACCTTGTG GTCTTAATCA GCTATATGCT ATGCAATATG GTACAGTTCC 1920
      TGTAGTTCAT GGAACTGGGG GCCTCCGAGA CACAGTCGAG ACCTTCAACC CTTTTGGTGC 1980
      AAAAGGAGAG GAGGGTACAG GGTGGGCGTT CTCACCGCTA ACCGTGGACA AGATGTTGTG 2040
 50   GGCATTGCGA ACCGCGATGT CGACATTCAG GGAGCACAAG CCGTCCTGGG AGGGGCTCAT 2100
      GAAGCGAGGC ATGACGAAAG ACCATACGTG GACCATGCC GCCGAGCAGT ACGAGCAGAT 2160
 55   CTTCGAATGG GCCTTCGTGG ACCAACCCTA CGTCATGTAG ACGGGGACTG GGGAGGTCGA 2220
      AGCGCGGGTC TCCTTGAGCT CTGAAGACAT GTTCCTCATC CTTCCGCGGC CCGGAAGGAT 2280
      ACCCCTGTAC ATTGCGTTGT CCTGCTACAG TAGAGTCGCA ATGCGCCTGC TTGCTTGGTC 2340
 60   CGCCGGTTCG AGAGTAGATG ACGGCTGTGC TGCTGCGGCG GTGACAGCTT CGGGTGGATG 2400
      ACAGTTACAG TTTTGGGGAA TAAGGAAGGG ATGTGCTGCA GGATGGTTAA CAGCAAAGCA 2460
 65   CCACTCAGAT GGCAGCCTCT CTGTCCGTGT TACAGCTGAA ATCAGAAACC AACTGGTGAC 2520
      TCTTTAGCCT TAGCGATTGT GAAGTTTGTT GCATTCTGTG TATGTTGTCT TGTCCTTAGC 2580
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TGACAAATAT TAGACCTGTT GGAGAATTTT ATTTATCTTT GCTGCTGTTG TTTTTGTTTT 2640

GTTAAAAAAA AAAAAAAAAA AA   2662

(2) INFORMATION FOR SEQ ID NO: 12:
  (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 768 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: protein

  (iii) HYPOTHETICAL: NO

  (vi) ORIGINAL SOURCE:
  (A) ORGANISM: triticum tauschii

  (ix) FEATURE:
  (A) NAME/KEY: Protein
  (B) LOCATION:1..768

  (ix) FEATURE:
  (A) NAME/KEY: Protein
  (B) LOCATION:1..768
  (D) OTHER INFORMATION:/product= "deduced amino acid
  sequence SBE II"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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Met Ala Thr Phe Ala Val Ser Gly Ala Thr Leu Gly Val Ala Arg Pro
1               5                   10                  15

Pro Ala Ala Ala Gln Pro Glu Glu Leu Gln Ile Pro Glu Asp Ile Glu
            20                  25                  30

Glu Gln Thr Ala Glu Val Asn Met Thr Gly Gly Thr Ala Glu Lys Leu
        35                  40                  45

Glu Ser Ser Glu Pro Thr Gln Gly Ile Val Glu Thr Ile Thr Asp Gly
        50                  55                  60

Val Thr Lys Gly Val Lys Glu Leu Val Val Gly Glu Lys Pro Arg Val
65                  70                  75                  80

Val Pro Lys Pro Gly Asp Gly Gln Lys Ile Tyr Glu Ile Asp Pro Thr
            85                  90                  95

Leu Lys Asp Phe Arg Ser His Leu Asp Tyr Arg Tyr Ser Glu Tyr Arg
            100                 105                 110

Arg Ile Arg Ala Ala Ile Asp Gln His Glu Gly Gly Leu Glu Ala Phe
        115                 120                 125

Ser Arg Gly Tyr Glu Lys Leu Gly Phe Thr Arg Ser Ala Glu Gly Ile
    130                 135                 140

Thr Tyr Arg Glu Trp Ala Pro Gly Ala His Ser Ala Ala Leu Val Gly
145                 150                 155                 160
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          Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Thr Met Thr Arg Asp Asp
                          165                 170                 175

 5        Tyr Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro
                          180                 185                 190

          Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser
                      195                 200                 205

10        Gly Val Lys Asp Ser Ile Ser Ala Trp Ile Lys Phe Ser Val Gln Ala
                      210                 215                 220

          Pro Gly Glu Ile Pro Phe Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu
          225                 230                 235                 240

15        Glu Lys Tyr Val Phe Gln His Pro Gln Pro Lys Arg Pro Glu Ser Leu
                          245                 250                 255

20        Arg Ile Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro Lys Ile
                          260                 265                 270

          Asn Ser Tyr Ala Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Arg
                      275                 280                 285

25        Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr
                290                 295                 300

          Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser
          305                 310                 315                 320

30        Arg Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His
                          325                 330                 335

          Glu Leu Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ser Ser
                      340                 345                 350

35        Asn Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His
                      355                 360                 365

          Tyr Phe His Gly Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg
          370                 375                 380

40        Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn
          385                 390                 395                 400

45        Ala Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp
                          405                 410                 415

          Gly Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln Met Thr Phe
                      420                 425                 430

50        Thr Gly Asn Tyr Gly Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala
                      435                 440                 445

          Val Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu His Pro
          450                 455                 460

55        Asp Ala Val Ser Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Cys
          465                 470                 475                 480

60        Ile Pro Val Pro Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met
                          485                 490                 495
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      Ala Val Ala Asp Lys Trp Ile Glu Leu Leu Lys Gln Ser Asp Glu Ser
                  500             505             510

 5    Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu
                  515             520             525

      Glu Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
          530             535             540

10    Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe
      545             550             555             560

      Met Ala Leu Asp Arg Pro Ser Thr Pro Arg Ile Asp Arg Gly Ile Ala
                  565             570             575

15    Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly Glu Gly
                  580             585             590

      Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp
20                595             600             605

      Phe Pro Arg Gly Pro Gln Thr Leu Pro Thr Gly Lys Val Leu Pro Gly
          610             615             620

25    Asn Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp
      625             630             635             640

      Ala Asp Phe Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met
                  645             650             655

30    Gln His Leu Glu Glu Lys Tyr Gly Phe Met Thr Ser Glu His Gln Tyr
                  660             665             670

      Val Ser Arg Lys His Glu Glu Asp Lys Val Ile Ile Phe Glu Arg Gly
35                675             680             685

      Asp Leu Val Phe Val Phe Asn Phe His Trp Ser Asn Ser Phe Phe Asp
          690             695             700

40    Tyr Arg Val Gly Cys Ser Arg Pro Gly Lys Tyr Lys Val Ala Leu Asp
      705             710             715             720

      Ser Asp Asp Ala Leu Phe Gly Gly Phe Ser Arg Leu Asp His Asp Val
                  725             730             735

45    Asp Tyr Phe Thr Thr Glu His Pro His Asp Asn Arg Pro Arg Ser Phe
                  740             745             750

      Ser Val Tyr Thr Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Thr Glu
50                755             760             765
```

(2) INFORMATION FOR SEQ ID NO: 13:
   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 10550 base pairs

55   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: both
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

60
   (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: triticum tauschii

(ix) FEATURE:
5   (A) NAME/KEY: exon
  (B) LOCATION:1..316
  (D) OTHER INFORMATION:/product= "exon 1"

(ix) FEATURE:
10   (A) NAME/KEY: exon
  (B) LOCATION:1472..1828
  (D) OTHER INFORMATION:/product= "exon 2"

(ix) FEATURE:
15   (A) NAME/KEY: exon
  (B) LOCATION:2766..2823
  (D) OTHER INFORMATION:/product= "exon 3"

(ix) FEATURE:
20   (A) NAME/KEY: exon
  (B) LOCATION:2906..3028
  (D) OTHER INFORMATION:/product= "exon 4"

(ix) FEATURE:
25   (A) NAME/KEY: exon
  (B) LOCATION:4113..4194
  (D) OTHER INFORMATION:/product= "exon 5"

(ix) FEATURE:
30   (A) NAME/KEY: exon
  (B) LOCATION:4286..4459
  (D) OTHER INFORMATION:/product= "exon 6"

(ix) FEATURE:
35   (A) NAME/KEY: exon
  (B) LOCATION:4562..4643
  (D) OTHER INFORMATION:/product= "exon 7"

(ix) FEATURE:
40   (A) NAME/KEY: exon
  (B) LOCATION:4744..4855
  (D) OTHER INFORMATION:/product= "exon 8"

(ix) FEATURE:
45   (A) NAME/KEY: exon
  (B) LOCATION:4999..5021
  (D) OTHER INFORMATION:/product= "exon 9"

(ix) FEATURE:
50   (A) NAME/KEY: exon
  (B) LOCATION:5102..5192
  (D) OTHER INFORMATION:/product= "exon 10"

(ix) FEATURE:
55   (A) NAME/KEY: exon
  (B) LOCATION:8593..8718

(D) OTHER INFORMATION:/product= "exon 11"

(ix) FEATURE:
(A) NAME/KEY: exon
5   (B) LOCATION:8807..8915
(D) OTHER INFORMATION:/product= "exon 12"

(ix) FEATURE:
(A) NAME/KEY: exon
10   (B) LOCATION:8992..9104
(D) OTHER INFORMATION:/product= "exon 13"

(ix) FEATURE:
(A) NAME/KEY: exon
15   (B) LOCATION:9161..9199
(D) OTHER INFORMATION:/product= "exon 14"

(ix) FEATURE:
(A) NAME/KEY: exon
20   (B) LOCATION:9498..9713
(D) OTHER INFORMATION:/product= "exon 15"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

25   ATGGCGGCGA CGGGCGTCGG CGCCGGGTGC CTCGCCCCCA GCGTCCGCCT   50

GCGCGCCGAT CCGGCGACGG CGGCCCGGGC GTCCGCTTGC GTCGTCCGCG   100

CGCGGCTCCG GCGCTTGGCG CGGGGCCGCT ACGTCGCCGA GCTCAGCAGG   150
30

GAGGGCCCCG CGGCGCGCCC CGCGCAGCAG CAGCAACTGG CCCCGCCGCT   200

CGTGCCAGGC TTCCTCGCGC CGCCGCCGCC CGCGCCCGCC CAGTCGCCGG   250

35   CCCCGACGCA GCCGCCCCTG CCGGACGCCG GCGTGGGGGA ACTCGCGCCC   300

GACCTCCTGC TCGAAGGTAA AAAACAAGGC TGAATCCTCA GATCACTCCG   350

CGTCTTCGTT TTACCAAATA CGGTACTGCG AAGTGGTGCT GTATATGTGA   400
40

AGTTTCTGTC GATTTCTTCC TGACGGATGT TCAGTCGATT CAGTTGTATA   450

TATGTGATAC GTTCGTTGTT CATCGATCGT ACAGATTTAC CAGCACACTA   500

45   GATAGAAATC GAGACCGACG CGGGCAGATC AATAGATTTT TCTAGACGTT   550

TTATTGGATC GTGAGATGAT TGATTGGGGT GGCGTGTCGA TACGATAGCG   600

GTGCACCGCC GATGTATCGG GGCATGTGCA CGTGGTTGGG TCTCAGCAGA   650
50

CATATCACTA GACTGGTATC GTAATTTACT AGTACTACTG GAAAGAGGAC   700

TAAAAAGGCT AGGCCAAGTG CACGCATGTT GGGAACGTTG TTAAATTGAT   750

55   GAGTTTGTCC TTTGCTTGGG CTGGTATTAT TACCAAAAAA TGGTGTTAGT   800

CCCTGTACTT ATTAATGGGA AAATCTTAAC ATGACACTGG GGTTTATGAG   850

TCTCCAATTG TATATTCTCA GCACTCAACT GATTTTACTG ATACTGTAGT   900

GGAAATGACA CGTGAGCACC CCCCTTCAAG GAATGCAATG CTTCTTTCTG   950

TTTTATATTA CAGGAACTAG AAGGAGCTTC CACCTTTGAG TACAGAAGTA   1000

CTCCCTCCGT TCCAAAATAG ATGACTCAAC TTTGTACTAA TTTTGTACTA   1050

TAGTTAGTAC AAAGTTGAGT CATCTATTTT AGAACGGAGG GAGTAGTATC   1100

GAAATTGAAG ACCCTTGTAT TACTGTCTTG TTTTTCAATG AAAATGGGAG   1150

GCCCATGCAG TAAGTCACAT GGGCACCTGG GAGGCTGGGA TCATGTGTGC   1200

TTTGCAGAGT ACTAGACCCA GCTCACCCTC TGTTAGATTA CTTGTTGGGC   1250

TGCTACTTTG TGTTTGCTGT GCAGTATATC AGACATCCTG AATTTGGCAT   1300

CTAGCTGAGA ACAGAATGCA GGTTGCACCA TTCTTATTAT TGCTAAACTG   1350

TTGTCACGCA ATTTATAAAG AATGTGATCT TCTGAGTATT AATTAATCAT   1400

GTTCTGCTAA TATCTGTCCT CGCTCTGGTG TTGACAAATA TACCATATGA   1450

ATATTTTCCA TTTTGCAACC AGGGATTGCT GAGGATTCCA TCGACAGCAT   1500

AATCGTGGCT GCAAGTGAGC AGGATTCTGA GATCATGGAT GCGAATGAGC   1550

AACCTCAAGC TAAAGTTACA CGTAGCATCG TGTTTGTGAC TGGTGAAGCT   1600

GCTCCTTATG CAAAGTCAGG GGGGCTGGGA GATGTTTGTG GTTCGTTACC   1650

AATTGCTCTT GCTGCTCGTG GTCACCGTGT GATGGTTGTA ATGCCAAGAT   1700

ACTTGAATGG GTCCTCTGAT AAAAACTATG CAAAGGCATT ATACACTGCG   1750

AAGCACATTA AGATTCCATG CTTTGGGGGA TCACATGAAG TGACCTTTTT   1800

TCATGAGTAT AGAGACAACG TCGATTGGGT GGGTACACAA TCACCTTCTT   1850

ATTCTCTGTT GAATTGTAGC AACTGTTTAT CCTTGTTTAC ACTTCTTTTA   1900

GCCCTGCAAA GACATATGTG ATTTCCATAC TTTTTTGTTA TTTCCCTTGT   1950

ACTCTTGCTC ATGAAGGTCA AAATATCATA TATCCATGGA AGTCATGCAT   2000

GTGCCTAGTA TTTTTGGTGT CGGTGCCTTT AACTTTCAGG GATTAATACG   2050

TGGAATTTGA TAACTAAAGT TTATTTTATT GAAAAAAATT GTAGGTTGG   2100

TGAGCCCACA GCCACGCAGT GGCACCACTG CTTGCACATG ATTTTGCATT   2150

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CCAATTTTAT TCTGCCAATT GCACTTAAGA GTATATACAT TTATCTTGGC   2250

CTCAATCATG GGAGTACTGT GCATTCAGTG CACCATCATT GTTCTAAGGA   2300

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AAATGGAATT GACATTAATG ATTGGAACCC CACCACAGAC AAGTGTCTCC   4800

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GTTTGCTTCC CATGATGTTC TCACTAACTA ATCCTATGTG GTTTGGCATA   4950

CTTGTCAGGC CAAATGTAAA GCTGAATTGC AGAAGGAGCT GGGTTTACCT   5000

GTAAGGGAGG ATGTTCCTCT GGTTAGATAC AAACCCCTAA GATATATATT   5050

TTTTAAATCC CTAAAAAAAA CTTGCCGATC ATCTCATTAG CTTGATTCAC   5100

AGATTGGCTT TATTGGAAGA CTGGATTACC AGAAAGGCAT TGATCTCATT   5150

AAAATGGCCA TTCCAGAGCT CATGAGGGAG GACGTGCAGT TTGTAAGTTC   5200

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GGCGAAGGAG GTGGAGGATA CCGGCTTCAA GCTGTGGTAC ATGGGACGGC   5800

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CGGTTAGGCA CGAAGGAAGG CGAAAGGGAC ATCTATAAGA TGGCCAAGAT   7200

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CAAGTGATGT CGACACTAAT GACTTCCCGA TTAAGATAGG ACTGCATCAG   8000

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TGGTGCTAGT TGACGATAGT CGGGCGGGGG TAAATAACAA GTTAGAGTTA   8150

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CGAGTACATG ATGTGCGGTT TCAGTACTAC TAGGTGTGAG GAGGAGGAGG   8250

- 93 -

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TTAGCCTTGA TGGGCAGGTG GTACCCCAGA AGGACACCTT TCGATATTTG        8300

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AATCAAAGCT GGATGGATGA AGTGGCGCCA AGCTTCTGGC ATTCTTTGTG        8400

ACAAGAGAGT GCCACAAAAG CTAAGGCAAG TTCTACAGGA CGGCGGTTCG        8450

ACCCGCAATG TTGTATGGCG CTGAGTGTTG GCCGACTAAA AGGCGACATG        8500

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CACACGAGGA AGRATCGAGT CCGGAATGAT GATATACGAG ATAGAGTTGG        8600

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ACTGGGGGCC TCCGAGTAAG ACAACTGCCT TGAAAATTAT CGTTATCTTG        9350

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GAGACCTTCA ACCCTTTTGG TGCAAAAGGA GAGGAGGGTA CAGGGTACGC        9450

ACTGCTCAAT TTTAGCTAAC TTTCAGTTTA TCTTTTTGCA ATGTCTTGGG        9500

GGTTCATTGC GCCATAAATC AACTTGTGAT AATTAACTGT TACTGTTCTG        9550

TACTTGCAGG TGGGCGTTCT CACCGCTAAC CGTGGACAAG ATGTTGTGGG        9600

TAAGTTTTTG CTGAGCTCTT GTCCGGTTAT AGGATCGACC TTGGCTGTAG        9650
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CATGGTACCT TAGTGCCCCT TGTATATAGA CCTAACCTGA TGGACTCACT   9700

TTGTCTACAC TAATCATAGT AGTCGATTGC CCGGAGGCGT TTTGCTTGGA   9750

TTCTGCTAAT TTAATTTTCA TGACGATAAC TCATACCATG GTTTGGTTCT   9800

CCGATGGGGG CCAGAATGGC GTCTAGTGTC TGCGATCTGT GTAACTAGCC   9850

5   AATGCCGGGT TGTTCCAAGT GAAAATTTAC CTTTTGACCA TTGTGCAGGC   9900

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10 AAGACATGTT CCTCATCCTT CCGCGGCCCG GAAGGATACC CCTGTACATT   10150

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15 AGCTGAAATC AGAAACCAAC TGGTGACTCT TTAGCCTTAG CGATTGTGAA   10400

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ACCTGTTGGA TAATTCTATC TTTGCTGCTG TTTTTCTTTT GGTCAAAAGA   10500

GGGGTTCCCT CCGATTTCAT TAACGAAACC ACCAAAATAA CAGCACCCAG   10550

TGCAGGTCTC AGGTTCAGAT ATACTTAAGA CTACTAAATC TAACAGCAGC   10600

20 TAAAAAGCTT AAAGATTCAG GCGACATAAC CGAACAAAAT CCACAACCGA   10650

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GCTGAAAAGG CAAGCAGACA GAGGTCTGCA TTCTGTCAAC ACCACTTGTG   10750

AAAAATGAAG AGAAGATCGA GAATTCCCGG GAATCCG   10787

(2) INFORMATION FOR SEQ ID NO: 14:
25   (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 647 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
30

        (ii) MOLECULE TYPE: protein

        (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: triticum tauschii
    (F) TISSUE TYPE: Endosperm

(ix) FEATURE:
    (A) NAME/KEY: Protein
    (B) LOCATION:1..647
    (D) OTHER INFORMATION:/product= "deduced amino acid
    sequence for SSS I"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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Met Ala Ala Thr Gly Val Gly Ala Gly Cys Leu Ala Pro Ser Val Arg
1             5                   10                  15

Leu Arg Ala Asp Pro Ala Thr Ala Ala Arg Ala Ser Ala Cys Val Val
            20                  25                  30

Arg Ala Arg Leu Arg Arg Leu Ala Arg Gly Arg Tyr Val Ala Glu Leu
        35                  40                  45

Ser Arg Glu Gly Pro Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala
    50                  55                  60

Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro Pro Pro Ala Pro Ala
65                  70                  75                  80

Gln Ser Pro Ala Pro Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly
            85                  90                  95

Glu Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile
            100                 105                 110

Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp
        115                 120                 125

Ala Asn Glu Gln Pro Gln Ala Lys Val Thr Arg Ser Ile Val Phe Val
    130                 135                 140

Thr Gly Glu Ala Ala Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val
145                 150                 155                 160

Cys Gly Ser Leu Pro Ile Ala Leu Ala Ala Arg Gly His Arg Val Met
            165                 170                 175

Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala
            180                 185                 190

Lys Ala Leu Tyr Thr Gly Lys His Ile Lys Ile Pro Cys Phe Gly Gly
        195                 200                 205

Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp
    210                 215                 220

Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly
225                 230                 235                 240

Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu
            245                 250                 255

Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr
            260                 265                 270
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              Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser
                      275                 280                 285
    5         Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr
                      290             295                 300
              Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly
                  305             310                 315                 320
   10         Leu Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp
                          325             330                 335
              Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala
                          340                 345                 350
   15         Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr
                      355                 360                 365
              Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr
   20             370                 375                 380
              Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys
                  385                 390                 395                 400
   25         Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn
                              405                 410                 415
              Pro Thr Thr Asp Lys Cys Leu Pro His His Tyr Ser Val Asp Asp Leu
   30                     420                 425                 430
              Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu
                      435                 440                 445
   35         Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp
                      450                 455                 460
              Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met
                  465                 470                 475                 480
   40         Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe
                              485                 490                 495
              Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg
   45                     500                 505                 510
              Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly
                      515                 520                 525
   50         Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn
                      530                 535                 540
              Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His Gly Thr
   55         545                 550                 555                 560
              Gly Gly Leu Arg Asp Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys
                              565                 570                 575
   60         Gly Glu Glu Gly Thr Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys
                          580                 585                 590
              Met Leu Trp Ala Leu Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys
                      595                 600                 605
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        Pro Ser Trp Glu Gly Leu Met Lys Arg Gly Met Thr Lys Asp His Thr
            610             615             620
5       Trp Asp His Ala Ala Glu Gln Tyr Glu Gln Ile Phe Glu Trp Ala Phe
            625             630             635             640

        Val Asp Gln Pro Tyr Val Met
                        645
10
        (2) INFORMATION FOR SEQ ID NO: 15:
          (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 5072 base pairs
          (B) TYPE: nucleic acid
15        (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

20        (iii) HYPOTHETICAL: NO

          (vi) ORIGINAL SOURCE:
          (A) ORGANISM: triticum tauschii
          (F) TISSUE TYPE: Endosperm
25        (ix) FEATURE:
          (A) NAME/KEY: promoter
          (B) LOCATION:1..4993
          (D) OTHER INFORMATION:/function= "region containing
          promoter of SSS I"
30
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

        TCTAGATGCA TGCTGGATAG CGGTCGATGT GTGGAGTAAT AGTAGTAGAT GCAGAATCGT      60
35      TTCGGTCTAC TTGTCGCGGA CGTGATGCCT ATATACATGA TCATACCTAG ATATTCTCAT     120
        AACTATGCTC AATTCTATCA ATTGCTCGAC AGTAATTCGT TTACCCACCG TAATACTTAT     180
        GATCTTGAGA GAAGTCACTA GTGAAACCTA TGCCCCCCAG GTCTATTTTG CATCATATTA     240
40      ATCTTCCAAT ACTTAGTTAT TTCCATTGCC GTTTATTTTA CTTTGTATCT TTATTTCTTT     300
        TTATTATAAA AAATACCAAA AATATTATCT TATCATATCT ATCAGATCTC ATTCTCGTAA     360
45      GTGACCGTGA AGGGATTGAC AACCCCTTTA TCGTGTTGGT TGCGAGGTTC TTGTTTGTTT     420
        GTGTAGGTGC GTGTGACTCG CACGTCTCCT ACTGGATTGA TACCTTGGGT TTTCAAAAAC     480
50      TGAGAAAAAT ACTTACGCTA CTTTACTGCA TAACCCTTTC CTCTTTAAAA AAAAAAACCA     540
        ACGTAGTATT CAAGAGGTAG CACGCTACCA TCCTCTCCAA CAGGAGCGCG AGATCTTTG      600
        TCCGGCAGGT TGATGCGGGC CGGGGAAGAA CTCCAGCTGC CTTGGCCAGC TTGGTCGTGA     660
55      GCCGCCCCAG CGGCGTCTTG AACCTGTCCA CGTAGCGCTC CCTGACACGC GGCGTGAACT     720
        GAGAAGGCTT GTCGATGAAC TCCAGCTGTT GTGCCAGCCT AGCTTGCGCC TTCTTCTGCT     780
        GGGTCATGCC CTTCGAGAAA CCCACCTTGG CCACCCTTGT GCTTGAGCGG CGCGCCACCT     840
60      CAGCAGGCGG CGGCGTGGGG ATGAAGAGGG TGTCTGCTTC CGGAGCAGGC GGGTCGGCGT     900
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      TGAACTTGAA AGGCGGTGGC CCCATGATGG ATGGGGGGAG CATGCCAAAG ACTTGGTTGA   960
      GGAAAGTGGT GTTGGCGTCC ACCTCCAGTG CCTGCAGTTT GGAAGCCAGA CGATTGGCGT  1020
  5   CGATCTCTGG CTCCGGCTGG AAGGAGGCTC GACGCTCCGG TGTGCCAGAA CGCAAAGGGA  1080
      GGAGCGGCAG CTCTGGCTGA GCAGACCCCG CGCCCATGTA CTCTGCATTG GGCCAAGGCT  1140
      GCAGGGGCAA GCCACCGGGA TGGGGGCGCG AGGTGGACTG CGCACCGGAG GAAGGCCAAG  1200
 10   CTCAACCTCG GTGAGGTTCG CCCCAGACCA GGGCGGCAGG CTCGGGTCCA CAAAGGGCCA  1260
      AACCGCCTCG TCCGCCCCGA AACTGTCCAG GACAGACGGC GGACGACGGA AGGCCGTGTC  1320
 15   GTCGAGCTCG AGCAGCAGAG GGTCCGTGCG GGTGATGTCT TGCCAAATGG ACTCCACCTC  1380
      CAGCAGGAAG GGGGACTGGT CCATCGCCCC TGGCCAAGCC ACTGGTACGC CAAAGATGGC  1440
      ATCAGCAGCG TTTGCACCAG GGGGAGCAGC CACACCTTGG AGGACAGGGA GGGTGCGGAC  1500
 20   GTCGACGGCA GCAAACGTG GCTGGAGCAA GTTGCCGTCG CGTGCCGGCC TCGGCGAGCG  1560
      CGAGCGGCTG TAGGAGCGCT CGGTGCCCTC AGACTCGGAC AGTGCGCCAG TGGGAGAGCC  1620
 25   ATGGCGACGC CGGCCACCAC TGGACGTGCC ATGGCGCTGG TCCTGACGGC GCCTGGATGG  1680
      CCCGTCCTCG CGGGCAGCTC CACCTGAGCG GCACCCGAGG AGCACACCCC GCCAAGCTGG  1740
 30   GCCAGGGCGG CTGCGGCGAC GGCGACGGCC GCGGTCGCGG TCTGCACCAT CATCTTCATC  1800
      TTCGTCATCG TGGCGCCTCG ACAAGGATG CTCGCTGTCA CCGACGCGAG GGACGTGAGC  1860
      CGGCTCAGCC CGCCCTTCCT CGACGTGGCG AGCCCTGCGG ATATGCTCCT CGAGCGGCCA  1920
 35   TTGGGGGTCG TTGGCGCGCG GCATCTCGGG GTCGCGGTCA GCTATCGGGG TGTAGTCCTT  1980
      TGTGGTGTCC AGGTGGATGA GCAGAGAGAA ATCCGGCCCC TCTAGCCCCT CGTCCCGGGG  2040
 40   GCAGCCCTCC GGCAGCGTCT GGCGGCCCCT GGGGTCCAGG GGTCGATCGA TGATGGAGAA  2100
      CCCCCTTTTG GTGGGGATGT CGTCCGGACT CCATGCCCAC ACCCAGGCAA AGAGGCAGGC  2160
      CGTGTTGGAG AGGGAGGTCG TCTGCCGCTC CAACCAGTCG ACGTGGCATG TCTTCCCGAG  2220
 45   CGCATCCTGC CCCGCCTCCT TGTTCCAGGA CTGCACCGGC ATGTTCTCGA CGGCGATGCG  2280
      GCAGTAGTAC CGCCAGACAC GGCGGTGGCC GTGTGCCGAT GGTGACCAGG CCGACAGGGA  2340
 50   GAGCGCGACG CCCCAGCAGG AGACGACCCC AGCGTCGAAA GCGATGTCCC GGTGCCTGAA  2400
      GTGGACGAGC CCAGAGATGG CCAGGCGCAT TGACGCGGGG AAGGGGAAGG AGTTAGGATG  2460
      GGCGACGCGG CCGGAGTGAA CCGCGGCGTG GTGGCCGACG GGGCTGGAGA GGCAGAGGCG  2520
 55   GAGTCATCCG AGAGAGGTGT ATCAGTGGCT CTGCACAATA CCCAGTGTCG CCACATCATA  2580
      TCCTGCTGAA TAACCACACA TGTGTACTGT CGTTAAATAA ATCATTGGTC ACGCGAACCC  2640
 60   GGAAAAAGAC GGCGAAAAAT TCACGGACAC ACGACTAGTA GTACCCAATA TACTCGGCAA  2700
      AAACAGTGAC ACGTCGTTTT GCGTTGTCGG CCGGTGTTGT CGAGTCATTG TACTATGTTT  2760
      TGTCGTTTCT TTCTTTTCTC CAAATCGACA AACCGTTTGT CTTTGGTTAA AAAACAGAAA  2820
 65   CATACAAAAT CAAATGAATG CATTCAAGGG CCGGTAATCC AATTCTGAGC CCAGGCTCAG  2880
      CTACACCCGC CCTTACAAAA AAATCAAAAT AAATACTAGA AAAATTCAAA AAATTCCAAT  2940
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     TTGTTTGTGC GTGGTAGATA ATTTGATGCG TGAGGTACGC TTCAATTTTC AAATTATTTG 3000

 5   GACATCTGAG CAGCTCTCAG CAAAAAAGAC AAATTCGGGG TCTGTAAAAA TGTTTACTGT 3060

     TCATGCACTG TTCTGACCCG ATTTGTCTTT TTTGCTGAGA GCTTCTCAGA AGTCCAAATG 3120

     AGCTAAAATT TTGAGCGGAG CTTACGTGAT AAAATGTCTA TCATGCAAAA AAGGATTGGA 3180

10   ATTTTTTGAA TTTTTTTTAT TTTTTGTGAT TTGTTTCCTG ACGGGTGCA GATAAGCCTG 3240

     GGCACCGAAA CGCCGCACTC AGGCTCATCC TTTTCTATAA AAGAAAAGAA ATACATACAA 3300

     TTTCCCTCTG TTTTTTGAGC AAGGGGCACC ACCCACCAAA GAGTTTTCAA CTCACATGGT 3360

15   ATTAGAGCAT CTACAGCCGG GCGTCTCAAA CCAGCCTCAT ACGCTTGAGC GGGTCGCCTT 3420

     GGTCACGATT TTTTGACCCA GACGGGCCCC TCAAACGGTC CTTAAACGCC CAGGCTGACC 3480

20   GACAACCCAC ATATCCAGCC CAAATATGGG GTGGATATGG GGGCGCCCGG GCACGCCAGC 3540

     CCGCGGACAC CACACATCTT CAGTTTCTAA TTTGAGATAT CCGGATGTGG AATGCGTTTT 3600

     TGAGGGGTGA CCGGTCCCTG TCCGTGGATG CGCCCGGACG TTTGAGGGGT TGGATTTGCC 3660

25   AAGTCTGATT AGAGATGCTC TTAGGTGTTC CACCCCCATC CCTTGATGGC TAGGGCAAAC 3720

     TCTCCCTCC AAACTTTGTC GGCGAGCCTG TGGATTCTTC TCTCCTCTGC CCGCTGCTCC 3780

30   GGCGGCTGAT GGCGGGGAGG AGAATCCCGG TGTCTTCGCT TGGTTAGTTG TTTAAGTTAC 3840

     GTACTTTTTT AGTCCTCGCA GGTGCGGCGT TCGGACGTAT GGTCGTGCTT CTTTTTTGAG 3900

     TTTGTCTTCC GGGCTCTGAT CCTCCTCGAG TTCGTCCATC TGGACGTACT CGACGGAGCT 3960

35   CCGGCATAGA TTCCTATCAT CGTCTTGGTG AGGTGAGGTT ATGGTTTCTT GTCATGTGGG 4020

     CAGATTTGGT GCCAGATGCT TCATATCTAT TCAAGGGTTC AGCGGCAACA ACTGCGGCTC 4080

40   CAGAGCGATG GTCCTTAAGG GCACGTGCAC GAAGACTTCA CGGCTGTTAT CGACAAGGTC 4140

     AAGCCGGCTC CGATAGGGGA GCAGCGACAG CGGCGCGTCA ACCGCTCGTT CTGGCGGCAG 4200

     TAGTGGTCGT TCGGTGCTCT CGGAACCTCG ATGTAATTTT TATGATTTTA GAGATGCTTT 4260

45   GTACTTCCGA TCGATGAACT CTGATAATAG ATATCTCTTC TCTCGCAAAA AAGAGAGTT 4320

     TTCAACTGAA AACAAAGAG TTTCACTAGT TCTTCTTTTA GAAACAGAGT TTCACTAGCA 4380

50   CTTTTTTTTG CGAGAAGTCG AGTTTCACTA AGTACTAAAC CCACGCAATT ATTCTCAAAA 4440

     AAAAAACCCA CGCAACTGTC TGGATCCATC TTCGTTTTTT CCCCGAGAAT CGTCTGGATC 4500

     CATTTTCGTG TGCGAGGCAT CCTCTCATTT TGCACGGCCC AGCTCTCTTC TCGCCGGCGT 4560

55   ACGCTGCTAC ATGTCGGCAC TCCACGCAAA CAAAAGAAG CCCAACCGAA AACGCACGCG 4620

     CCTTTCCAGG CTCACCACGG AAAAAAATAC CACGCCGC TCACGAGCAA ACCGTGACAA 4680

60   CAGCCAGCCA GATATGGCAA CGGAGGCACG GGCCGCACAC AGCCACTGAA AACCGCAGCT 4740

     GCTCTTCCGT CCGTCCGTCC CTCCGCCCGT CCGCGCCACT CCACTCGCCT TGCCCCACTC 4800

     CCACTCTTCT CTCCCCGCGC ACACCGAGTC GGCACCGGCT CATCACCCAT CACCTCGGCC 4860

65   TCGGCCACCG GCAAACCCCC CGATCCGCTT TTGCAGGCAG CGCACTAAAA CCCCGGGGAG 4920
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CGCGCCCCGC GGCAGCAGCA GCACCGCAGT GGGAGAGAGA GGCTTCGCCC CGGCCCGCAC 4980

CGAGCGGGGC GATCCACCGT CCGTGCGTCC GCACCTCCTC CGCCTCCTCC CCTGTCCCGC 5040

GCGCCCACAC CCATGGCGGC GACGGGCGTC GG   5072

(2) INFORMATION FOR SEQ ID NO: 16:
   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 1706 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

   (vi) ORIGINAL SOURCE:
   (A) ORGANISM: triticum tauschii
   (F) TISSUE TYPE: Endosperm

   (ix) FEATURE:
   (A) NAME/KEY: CDS
   (B) LOCATION:1..1706
   (D) OTHER INFORMATION:/product= "partial cDNA for
   hexaploid wheat DBE"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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GCT GTG TCG AAG CTT GAC TAT TTG AAG GAG CTT GGA GTT AAT TGT ATT    48
Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu Leu Gly Val Asn Cys Ile
 1               5                  10                  15

GAA TTA ATG CCC TGC CAT GAG TTC AAC GAG CTG GAG TAC TCA ACC TCT    96
Glu Leu Met Pro Cys His Glu Phe Asn Glu Leu Glu Tyr Ser Thr Ser
                20                  25                  30

TCT TCC AAG ATG AAC TTT TGG GGA TAT TCT ACC ATA AAC TTC TTT TCA   144
Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser Thr Ile Asn Phe Phe Ser
            35                  40                  45

CCA ATG ACG AGA TAC ACA TCA GGC GGG ATA AAA AAC TGT GGG CGT GAT   192
Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile Lys Asn Cys Gly Arg Asp
        50                  55                  60

GCC ATA AAT GAG TTC AAA ACT TTT GTA AGA GAG GCT CAC AAA CGG GGA   240
Ala Ile Asn Glu Phe Lys Thr Phe Val Arg Glu Ala His Lys Arg Gly
 65                  70                  75                  80

ATT GAG GTG ATC CTG GAT GTT GTC TTC AAC CAT ACA GCT GAG GGT AAT   288
Ile Glu Val Ile Leu Asp Val Val Phe Asn His Thr Ala Glu Gly Asn
                85                  90                  95

GAG AAT GGT CCA ATA TTA TCA TTT AGG GGG GTC GAT AAT ACT ACA TAC   336
Glu Asn Gly Pro Ile Leu Ser Phe Arg Gly Val Asp Asn Thr Thr Tyr
            100                 105                 110

TAT ATG CTT GCA CCC AAG GGA GAG TTT TAT AAC TAT TCT GGC TGT GGG   384
Tyr Met Leu Ala Pro Lys Gly Glu Phe Tyr Asn Tyr Ser Gly Cys Gly
            115                 120                 125
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      AAT ACC TTC AAC TGT AAT CAT CCT GTG GTT CGT CAA TTC ATT GTA GAT    432
      Asn Thr Phe Asn Cys Asn His Pro Val Val Arg Gln Phe Ile Val Asp
          130             135             140

  5   TGT TTA AGA TAC TGG GTG ATG GAA ATG CAT GTT GAT GGT TTT CGT TTT    480
      Cys Leu Arg Tyr Trp Val Met Glu Met His Val Asp Gly Phe Arg Phe
      145             150             155             160

 10   GAT CTT GCA TCC ATA ATG ACC AGA GGT TCC AGT CTG TGG GAT CCA GTT    528
      Asp Leu Ala Ser Ile Met Thr Arg Gly Ser Ser Leu Trp Asp Pro Val
                  165             170             175

 15   AAC GTG TAT GGA GCT CCA ATA GAA GGT GAC ATG ATC ACA ACA GGG ACA    576
      Asn Val Tyr Gly Ala Pro Ile Glu Gly Asp Met Ile Thr Thr Gly Thr
                  180             185             190

      CCT CTT GTT ACT CCA CCA CTT ATT GAC ATG ATC AGC AAT GAC CCA ATT    624
      Pro Leu Val Thr Pro Pro Leu Ile Asp Met Ile Ser Asn Asp Pro Ile
                  195             200             205
 20
      CTT GGA GGC GTC AAG CTC ATT GCT GAA GCA TGG GAT GCA GGA GGC CTC    672
      Leu Gly Gly Val Lys Leu Ile Ala Glu Ala Trp Asp Ala Gly Gly Leu
          210             215             220

 25   TAT CAA GTA GGT CAA TTC CCT CAC TGG AAT GTT TGG TCT GAG TGG AAT    720
      Tyr Gln Val Gly Gln Phe Pro His Trp Asn Val Trp Ser Glu Trp Asn
      225             230             235             240

      GGG AAG TAC CGG GAC ATT GTG CGC CAA TTC ATT AAA GGC ACT GAT GGA    768
 30   Gly Lys Tyr Arg Asp Ile Val Arg Gln Phe Ile Lys Gly Thr Asp Gly
                  245             250             255

      TTT GCT GGT GGT TTT GCC GAA TGT CTT TGT GGA AGT CCA CAC CTA TAC    816
      Phe Ala Gly Gly Phe Ala Glu Cys Leu Cys Gly Ser Pro His Leu Tyr
 35               260             265             270

      CAG GCA GGA GGA AGG AAA CCT TGG CAC AGT ATC AAC TTT GTA TGT GCA    864
      Gln Ala Gly Gly Arg Lys Pro Trp His Ser Ile Asn Phe Val Cys Ala
                  275             280             285
 40
      CAT GAT GGA TTT ACA CTG GGT GAT TTG GTA ACA TAT AAT AAC AAG TAC    912
      His Asp Gly Phe Thr Leu Gly Asp Leu Val Thr Tyr Asn Asn Lys Tyr
          290             295             300

 45   AAT TTA CCA AAT GGG GAG AAC AAT AGA GAT GGA GAA AAT CAC AAT CTT    960
      Asn Leu Pro Asn Gly Glu Asn Asn Arg Asp Gly Glu Asn His Asn Leu
      305             310             315             320

 50   AGC TGG AAT TGT GGG GAG GAA GGA GAA TTC GCA AGA TTG TCT GTC AAA   1008
      Ser Trp Asn Cys Gly Glu Glu Gly Glu Phe Ala Arg Leu Ser Val Lys
                  325             330             335

      AGA TTG AGG AAG AGG CAG ATG CGC AAT TTC TTT GTT TGT CTC ATG GTT   1056
      Arg Leu Arg Lys Arg Gln Met Arg Asn Phe Phe Val Cys Leu Met Val
 55               340             345             350

      TCT CAA GGA GTT CCA ATG TTT TAC ATG GGC GAT GAA TAT GGC CAC ACA   1104
      Ser Gln Gly Val Pro Met Phe Tyr Met Gly Asp Glu Tyr Gly His Thr
                  355             360             365
 60
      AAA GGG GGC AAC AAC AAT ACA TAC TGC CAT GAT TCT TAT GTC AAT TAT   1152
      Lys Gly Gly Asn Asn Asn Thr Tyr Cys His Asp Ser Tyr Val Asn Tyr
          370             375             380
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      TTT CGC TGG GAT AAA AAA GAA CAA TAC TCT GAC TTG CAC AGA TTC TGC   1200
      Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser Asp Leu His Arg Phe Cys
 5    385               390               395               400

      TGC CTC ATG ACC AAA TTC CGC AAG GAG TGC GAG GGT CTT GGC CTT GAG   1248
      Cys Leu Met Thr Lys Phe Arg Lys Glu Cys Glu Gly Leu Gly Leu Glu
                        405               410               415
10
      GAC TTT CCA ACG GCC GAA CGG CTG CAG TGG CAT GGT CAT CAG CCT GGG   1296
      Asp Phe Pro Thr Ala Glu Arg Leu Gln Trp His Gly His Gln Pro Gly
                        420               425               430

      AAG CCT GAT TGG TCT GAG AAT AGC CGA TTC GTT GCC TTT TCC ATG AAA   1344
15    Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe Val Ala Phe Ser Met Lys
                        435               440               445

      GAT GAA AGA CAG GGC GAG ATC TAT GTG GCC TTC AAC ACC AGC CAC TTA   1392
      Asp Glu Arg Gln Gly Glu Ile Tyr Val Ala Phe Asn Thr Ser His Leu
20    450               455               460

      CCG GCC GTT GTT GAG CTC CCA GAG CGC GCA GGG CGC CGG TGG GAA CCG   1440
      Pro Ala Val Val Glu Leu Pro Glu Arg Ala Gly Arg Arg Trp Glu Pro
25    465               470               475               480

      GTG GTG GAC ACA GGC AAG CCA GCA CCA TAT GAC TTC CTC ACC GAC GAC   1488
      Val Val Asp Thr Gly Lys Pro Ala Pro Tyr Asp Phe Leu Thr Asp Asp
                        485               490               495
30
      TTA CCT GAT CGC GCT CTC ACC ATA CAC CAG TTC TCT CAT TTC CTC AAC   1536
      Leu Pro Asp Arg Ala Leu Thr Ile His Gln Phe Ser His Phe Leu Asn
                        500               505               510

      TCC AAC CTC TAC CCC ATG CTC AGC TAC TCA TCG GTC ATC CTA GTA TTG   1584
35    Ser Asn Leu Tyr Pro Met Leu Ser Tyr Ser Ser Val Ile Leu Val Leu
                        515               520               525

      CGC CCT GAT GTT TGA GAG ACA AAT ATA TAC AGT AAA TAA TAT GTC TAT   1632
      Arg Pro Asp Val  *  Glu Thr Asn Ile Tyr Ser Lys  *  Tyr Val Tyr
40    530               535               540

      ATG TAG TCC TTT GGC GTA TTA TCA GTG TGC ACA ATT GCT CTA TTG CCA   1680
      Met  *  Ser Phe Gly Val Leu Ser Val Cys Thr Ile Ala Leu Leu Pro
      545               550               555               560
45
      GTG ATC TAT TCG ATA GCG GCC GCG  AA                               1706
      Val Ile Tyr Ser Ile Ala Ala Ala
      565
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(A) ORGANISM: triticum tauschii
(F) TISSUE TYPE: Endosperm

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..9289
(D) OTHER INFORMATION:/product= "genomic sequence of DBE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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CGG GAC CGT CCC TTG GCA ACT TGG GTT ACG TTG GGA CCT GAC GCT TCG     48
Arg Asp Arg Pro Leu Ala Thr Trp Val Thr Leu Gly Pro Asp Ala Ser
    570             575             580

CTT ATC CGG TGT GCC CTG AGA CGA GAT ATG TGC AGC TCC TAT CGG ATT     96
Leu Ile Arg Cys Ala Leu Arg Arg Asp Met Cys Ser Ser Tyr Arg Ile
585             590             595             600

TGT CGG CAC ATT CGG CGG CTT TGC TGG TCT TGT TTT ACC ATT GTC GAA    144
Cys Arg His Ile Arg Arg Leu Cys Trp Ser Cys Phe Thr Ile Val Glu
            605             610             615

ATG TCT TAT AAA CCG GGA TTC CGA GAC TGA TCG GGT CTT CCC GGG AGA    192
Met Ser Tyr Lys Pro Gly Phe Arg Asp  *  Ser Gly Leu Pro Gly Arg
            620             625             630

AGG TTT ATC CTT CGT TGA CCG TGA GAG CTT ATA ATG GGC TAA GTT GGG    240
Arg Phe Ile Leu Arg  *  Pro  *  Glu Leu Ile Met Gly  *  Val Gly
            635             640             645

ACA CCC CTG CAG GGT ATT ATC TTT CGA AAG CCG TGC CCG CGG TTA TGA    288
Thr Pro Leu Gln Gly Ile Ile Phe Arg Lys Pro Cys Pro Arg Leu  *
            650             655             660

GGC AGA TGG GAA TTT GTT AAT GTC CGA TTG TAG AGA ACC TGT CAC TTG    336
Gly Arg Trp Glu Phe Val Asn Val Arg Leu  *  Arg Thr Cys His Leu
665             670             675             680

ACT TAA TTT AAA ATT CAT CAA CCG TGT GTG TAG CCG TGA TGG TCT CTT    384
Thr  *  Phe Lys Ile His Gln Pro Cys Val  *  Pro  *  Trp Ser Leu
            685             690             695

TTC GGC GGA GTC CGG GAA GTG AAC ACG GTT TGA GTT ATG CAT GAA CGT    432
Phe Gly Gly Val Arg Glu Val Asn Thr Val  *  Val Met His Glu Arg
            700             705             710

AAG TAG TTT CAG GAT CAC TCC TTG ATC ACT TCT AGC TCC GCG ACC GTT    480
Lys  *  Phe Gln Asp His Ser Leu Ile Thr Ser Ser Ser Ala Thr Val
            715             720             725

GCG TTG TTT CTC TTC TCG CTC TCA TTT GCG TAT GTT AGC CAC CAT ATA    528
Ala Leu Phe Leu Phe Ser Leu Ser Phe Ala Tyr Val Ser His His Ile
            730             735             740

TGC TTA GTG TCT GCT GCA GCT CCA CCT CAT TAC CCC TTC CTT TCC TAT    576
Cys Leu Val Ser Ala Ala Ala Pro Pro His Tyr Pro Phe Leu Ser Tyr
745             750             755             760

AAG CTT AAA TAG TCT TGA TCT CGC GGG TGT GAG ATT GCT GAG TCC TCG    624
Lys Leu Lys  *  Ser  *  Ser Arg Gly Cys Glu Ile Ala Glu Ser Ser
            765             770             775
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     TGA CTT ACA GAT TCT ACC AAA ACA GTT GCA GGT GTC GAC GAT GCC AGT    672
      *  Leu Thr Asp Ser Thr Lys Thr Val Ala Gly Val Asp Asp Ala Ser
             780             785             790

 5   GCA GGT GAC GCA ACC GAG CTC AAG TGG GAG TTC GAC GAG GAA CGT GGT    720
     Ala Gly Asp Ala Thr Glu Leu Lys Trp Glu Phe Asp Glu Glu Arg Gly
             795             800             805

     CGT TAC TAT GTT TCT TTT CCT GAT GAT CAG TAG TGG AGC CCA GTT GGG    768
10   Arg Tyr Tyr Val Ser Phe Pro Asp Asp Gln  *  Trp Ser Pro Val Gly
             810             815             820

     ACG ATC GGG GAT CTA GCA TTT GGG GTT ATC TTA ATT TCT TTT AGA TTT    816
15   Thr Ile Gly Asp Leu Ala Phe Gly Val Ile Leu Ile Ser Phe Arg Phe
     825             830             835             840

     GAC CGT AAT CGG TCT ATG TGT GGA TTT TGG ATG ATG TAT GAA TTA TTT    864
     Asp Arg Asn Arg Ser Met Cys Gly Phe Trp Met Met Tyr Glu Leu Phe
             845             850             855
20

     ATG TAT TGT GTG AAG TGG CGA TTG TAA GCC AAC TCT CGT TAT CCC ATT    912
     Met Tyr Cys Val Lys Trp Arg Leu  *  Ala Asn Ser Arg Tyr Pro Ile
             860             865             870

25   CTT GTT CAT TAC ATG GGA TTG TGT GAA GAT GAC CCT TCT TGC GAC AAA    960
     Leu Val His Tyr Met Gly Leu Cys Glu Asp Asp Pro Ser Cys Asp Lys
             875             880             885

     ACC ACA ATG CGG TTA TGC CTC TAA GTC GTG CCT CGA CAC GTG GGA GAT   1008
30   Thr Thr Met Arg Leu Cys Leu  *  Val Val Pro Arg His Val Gly Asp
             890             895             900

     ATA GCC GCA TCG TGG GCG TTA CAC GCA AGT CTT CAT AGC AAC CAA AAC   1056
35   Ile Ala Ala Ser Trp Ala Leu His Ala Ser Leu His Ser Asn Gln Asn
     905             910             915             920

     TCC TCT CCG CAT TAC AAG CCA CCA ATC GCA GCC ACC ATG ACT TTC TTC   1104
     Ser Ser Pro His Tyr Lys Pro Pro Ile Ala Ala Thr Met Thr Phe Phe
             925             930             935
40

     ACC ACT GTC AAT GCC ATG AAA ATC TAT ATG TAG ACA TGT CCC ATT GCA   1152
     Thr Thr Val Asn Ala Met Lys Ile Tyr Met  *  Thr Cys Pro Ile Ala
             940             945             950

45   TCG GCA AGA AAG CGA AGC TTC ACG GCA CAC CTT CAT GAA GCC TCT CTG   1200
     Ser Ala Arg Lys Arg Ser Phe Thr Ala His Leu His Glu Ala Ser Leu
             955             960             965

     GCC GAA GAC AAG GAT GCG CCC GAC CGG ATC AAT TCC TAT CTA GAT ACC   1248
50   Ala Glu Asp Lys Asp Ala Pro Asp Arg Ile Asn Ser Tyr Leu Asp Thr
             970             975             980

     TAG TGG AGC CAT GCG CCA ATA GCG GAG ATC TCC GAG AGG AAG ACC GGA   1296
55    *  Trp Ser His Ala Pro Ile Ala Glu Ile Ser Glu Arg Lys Thr Gly
     985             990             995            1000

     ACT CGT CGG ACG TCG GCG TCC AAA TCG AGG AGG CCG GCA TGA AGC ACA   1344
     Thr Arg Arg Thr Ser Ala Ser Lys Ser Arg Arg Pro Ala  *  Ser Thr
            1005            1010            1015
60

     TCG AGG ATG GTG ATC CCC ATA CGG GTA GAT CGG GTC GGC CGC CAT CTC   1392
     Ser Arg Met Val Ile Pro Ile Arg Val Asp Arg Val Gly Arg His Leu
            1020            1025            1030
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     ACA CCG AGA TTA GGA TGC TTA AAA CGG TTT TTT TGG CAC TAG CAT TAT    1440
     Thr Pro Arg Leu Gly Cys Leu Lys Arg Phe Phe Trp His  *  His Tyr
             1035                 1040                 1045

 5   TTT GCA TCA TCC GTT GGA GAG AAC ATG AGA GAG CCC CAT TTC TTC CAC    1488
     Phe Ala Ser Ser Val Gly Glu Asn Met Arg Glu Pro His Phe Phe His
             1050                 1055                 1060

10   GGT TCT ACC TAT GGG ATC TTG TTC TGC TTG CAA CCG GGC CTC ACG GAA    1536
     Gly Ser Thr Tyr Gly Ile Leu Phe Cys Leu Gln Pro Gly Leu Thr Glu
             1065             1070             1075             1080

     AAC CCG CGC CAG CGG ACC CAC CCC ATG CTA GCA GGG CAC GGC ACC CGC    1584
     Asn Pro Arg Gln Arg Thr His Pro Met Leu Ala Gly His Gly Thr Arg
15                       1085             1090             1095

     AGC GGC CGG TCC AAA TGG ACG GTG AGA ACC GCA ACG CGA CAC GCC CGG    1632
     Ser Gly Arg Ser Lys Trp Thr Val Arg Thr Ala Thr Arg His Ala Arg
                 1100             1105             1110
20

     CAC TGT CAG CAA AGC GAG AGC GCG CGC ACG GCA CAC GCA CGC TCG GAC    1680
     His Cys Gln Gln Ser Glu Ser Ala Arg Thr Ala His Ala Arg Ser Asp
             1115             1120             1125

25   GAA CGG ACG GTG CGA TCG ATC CCT CCC CCC TCG CTC AAC CAC AGT AGT    1728
     Glu Arg Thr Val Arg Ser Ile Pro Pro Pro Ser Leu Asn His Ser Ser
             1130             1135             1140

     ACC CTG CCA CAC TAT CAC GCA CGC ACT CGA GTC ACA CCT CCC ACG AAG    1776
30   Thr Leu Pro His Tyr His Ala Arg Thr Arg Val Thr Pro Pro Thr Lys
             1145             1150             1155             1160

     AAC CAA CAG GAG GCG CGG ATC CCA CCG ATA AAT AAC CCC GCC TCG CCG    1824
     Asn Gln Gln Glu Ala Arg Ile Pro Pro Ile Asn Asn Pro Ala Ser Pro
35                       1165             1170             1175

     CTC CTC CCC AAA ATC AAT CAC CGA TCG CTC GGG GTT CCC GGC ATG ACG    1872
     Leu Leu Pro Lys Ile Asn His Arg Ser Leu Gly Val Pro Gly Met Thr
                 1180             1185             1190
40

     ATG ATG GCC ATG GCC AAG GCG CCC TGC CTC TGC GCG CGC CCG TCC CTC    1920
     Met Met Ala Met Ala Lys Ala Pro Cys Leu Cys Ala Arg Pro Ser Leu
             1195             1200             1205

45   GCC GCG CGC GCG AGG CGG CCG GGG CCG GGG CCG GCG CCG CGC CTG CGA    1968
     Ala Ala Arg Ala Arg Arg Pro Gly Pro Gly Pro Ala Pro Arg Leu Arg
             1210             1215             1220

     CGG TGG CGA CCC AAT GCG ACG GCG GGG AAG GGG GTC GGC GAG GTG TGC    2016
50   Arg Trp Arg Pro Asn Ala Thr Ala Gly Lys Gly Val Gly Glu Val Cys
     1225                 1230             1235             1240

     GCC GCG GTT GTC GAG GCG GCG ACG AAG GCC GAG GAT GAG GAC GAC GAC    2064
     Ala Ala Val Val Glu Ala Ala Thr Lys Ala Glu Asp Glu Asp Asp Asp
55                       1245             1250             1255

     GAG GAG GAG GCG GTG GCG GAG GAC AGG TAC GCG CTC GGC GGC GCG TGC    2112
     Glu Glu Glu Ala Val Ala Glu Asp Arg Tyr Ala Leu Gly Gly Ala Cys
                 1260             1265             1270
60

     AGG GTG CTC GCC GGA ATG CCC GCG CCG CTG GGC GCC ACC GCG CTC GCC    2160
     Arg Val Leu Ala Gly Met Pro Ala Pro Leu Gly Ala Thr Ala Leu Ala
             1275             1280             1285
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GGC GGG GTC AAT TTC GCC GTC TAC TCC GGT GGA GCC ACC GCC GCG GCG      2208
Gly Gly Val Asn Phe Ala Val Tyr Ser Gly Gly Ala Thr Ala Ala Ala
    1290                1295                1300

CTC TGC CTC TTC ACG CCA GAA GAT CTC AAG GCG GTG GGG TTG CCT CCC      2256
Leu Cys Leu Phe Thr Pro Glu Asp Leu Lys Ala Val Gly Leu Pro Pro
1305                1310                1315                1320

GAG TAG AGT TCA TCA GCT TTG CGT GCG CCG CGC GCC CCC TTT TCT GGC      2304
Glu  *  Ser Ser Ser Ala Leu Arg Ala Pro Arg Ala Pro Phe Ser Gly
                1325                1330                1335

CTG CGA TTT AAG TTT TGT ACT GGG GGA AAT GCT GCA GGA TAG GGT GAC      2352
Leu Arg Phe Lys Phe Cys Thr Gly Gly Asn Ala Ala Gly  *  Gly Asp
                1340                1345                1350

GGA GGA GGT TTC CCT TGA CCC CCT GAT GAA TCG GAC TGG GAA CGT GTG      2400
Gly Gly Gly Phe Pro  *  Pro Pro Asp Glu Ser Asp Trp Glu Arg Val
                1355                1360                1365

GCA TGT CTT CAT TGA AGG CGA GCT GCA CGA CAT GCT TTA CGG GTA CAG      2448
Ala Cys Leu His  *  Arg Arg Ala Ala Arg His Ala Leu Arg Val Gln
    1370                1375                1380

GTT CGA CGG CAC CTT TGC TCC TCA CTG CGG GCA CTA CCT TGA TAT TTC      2496
Val Arg Arg His Leu Cys Ser Ser Leu Arg Ala Leu Pro  *  Tyr Phe
1385                1390                1395                1400

CAA TGT CGT GGT GGA TCC TTA TGC TAA GGT GAT CAT ACT TTA GCT TTA      2544
Gln Cys Arg Gly Gly Ser Leu Cys  *  Gly Asp His Thr Leu Ala Leu
                1405                1410                1415

CCT GCA TCT TGG TAT TTA CAG TAG AAA TTG TTA CGT GGA CCC TTA TTT      2592
Pro Ala Ser Trp Tyr Leu Gln  *  Lys Leu Leu Arg Gly Pro Leu Phe
                1420                1425                1430

GTT GCC TTT TGT GTT GCT CTA GGC AGT GAT AAG CCG AGG GGA GTA TGG      2640
Val Ala Phe Cys Val Ala Leu Gly Ser Asp Lys Pro Arg Gly Val Trp
                1435                1440                1445

CGT TCC GGC GCG TGG TAA CAA TTG CTG GCC TCA GAT GGC TGG CAT GAT      2688
Arg Ser Gly Ala Trp  *  Gln Leu Leu Ala Ser Asp Gly Trp His Asp
    1450                1455                1460

CCC TCT TCC ATA TAG CAC GGT ATG CCT GAT TGC TGA AAA TAT TGG CTG      2736
Pro Ser Ser Ile  *  His Gly Met Pro Asp Cys  *  Lys Tyr Trp Leu
1465                1470                1475                1480

CAT TTG TTT CTC TCT TTT TCT CAT ATT TTT CTC CTG TCT TTC ACT TGT      2784
His Leu Phe Leu Ser Phe Ser His Ile Phe Leu Leu Ser Phe Thr Cys
                1485                1490                1495

ACT ACA TTG CCT CAG ACA GTC ATG ATC AAA GAG AGC AGT GTC ATT AGA      2832
Thr Thr Leu Pro Gln Thr Val Met Ile Lys Glu Ser Ser Val Ile Arg
                1500                1505                1510

CAT TTG TAG TTG TCT GCT GAC TTT GAC CAA AAC TTG TAA TTT ACT GTT      2880
His Leu  *  Leu Ser Ala Asp Phe Asp Gln Asn Leu  *  Phe Thr Val
            1515                1520                1525

GTT AAA GGT CCT TGA ATC ATA TTT TTT TAT AAT ATT ATG TTT GCA AGT      2928
Val Lys Gly Pro  *  Ile Ile Phe Phe Tyr Asn Ile Met Phe Ala Ser
            1530                1535                1540
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GGA AGT AAA GTG AAA TTG CAT CTA GTA TTT GTT GTT GCT GTC TTA GTC    2976
Gly Ser Lys Val Lys Leu His Leu Val Phe Val Val Ala Val Leu Val
1545            1550             1555             1560
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 5  GTT TAA TTG GAC ATG CAG TAA AAA GGT TTG CAT CTG CAG TTT GAT TGG    3024
    Val  *  Leu Asp Met Gln  *  Lys Gly Leu His Leu Gln Phe Asp Trp
                 1565             1570             1575
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```
10  GAA GGC GAC CTA CCT CTA AGA TAT CCT CAA AAG GAC CTG GTA ATA TAT    3072
    Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr
                 1580             1585             1590
```

```
    GAG ATG CAC TTG CGT GGA TTC ACG AAG CAT GAT TCA AGC AAT GTA GAA    3120
    Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu
15           1595             1600             1605
```

```
    CAT CCG GGT ACT TTC ATT GGA GCT GTG TCG AAG CTT GAC TAT TTG AAG    3168
    His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys
             1610             1615             1620
20
    GTA CAG CTG TAC TTG CTG ACT ACA TAG GAT AAT TTT TAA AGA AAG CTA    3216
    Val Gln Leu Tyr Leu Leu Thr Thr  *  Asp Asn Phe  *  Arg Lys Leu
    1625             1630             1635             1640
```

```
25  CAT ATT AGC CAG AAT TTG GGT TAT TAC AAA AAC TAC TGC ATA CTA TAG    3264
    His Ile Ser Gln Asn Leu Gly Tyr Tyr Lys Asn Tyr Cys Ile Leu  *
                 1645             1650             1655
```

```
    CAG TTA CAT GCT CAT TAT CGA GGA GAT GCT CAC ACG CAT CTT ATT TGG    3312
30  Gln Leu His Ala His Tyr Arg Gly Asp Ala His Thr His Leu Ile Trp
                 1660             1665             1670
```

```
    ATT TAA TAC CCA ATT CTG TTT TGA TAT TGG ACT GTT CCC TCT ACA GGA    3360
    Ile  *  Tyr Pro Ile Leu Phe  *  Tyr Trp Thr Val Pro Ser Thr Gly
35           1675             1680             1685
```

```
    GCT TGG AGT TAA TTG TAT TGA ATT AAT GCC CTG CCA TGA GTT CAA CGA    3408
    Ala Trp Ser  *  Leu Tyr  *  Ile Asn Ala Leu Pro  *  Val Gln Arg
    1690             1695             1700
40
    GCT GGA GTA CTC AAC CTC TTC TTC CAA GTA AGG ACA TGA ATT TAG TAT    3456
    Ala Gly Val Leu Asn Leu Phe Phe Gln Val Arg Thr  *  Ile  *  Tyr
    1705             1710             1715             1720
```

```
45  TAG CCT GCC AGC ACT GTT TGA GTG AGA GTT CAT ACA CAT TTT GTG CCT    3504
     *  Pro Ala Ser Thr Val  *  Val Arg Val His Thr His Phe Val Pro
                 1725             1730             1735
```

```
    GCA TAA CTG ATA TTT GTT CAA ACT ATT TTT TTT AGC AGT CAC TCA ACA    3552
50  Ala  *  Leu Ile Phe Val Gln Thr Ile Phe Phe Ser Ser His Ser Thr
                 1740             1745             1750
```

```
    GTT TTA CAT ATA TAT ATA ATA TAG ACT ATT CGT CAC CCT GGG TGA GGA    3600
    Val Leu His Ile Tyr Ile Ile  *  Thr Ile Arg His Pro Gly  *  Gly
55           1755             1760             1765
```

```
    ATA GTT ATT CTT CAC CCA CCT CTA TTT TAA CAT CTA TGC ACC GTA ATT    3648
    Ile Val Ile Leu His Pro Pro Leu Phe  *  His Leu Cys Thr Val Ile
    1770             1775             1780
60
    TTA CGT TTC GTA AAT TTG TCT TAT TTT AGA GAT AAA AAG AGA ACG TAA    3696
    Leu Arg Phe Val Asn Leu Ser Tyr Phe Arg Asp Lys Lys Arg Thr  *
    1785             1790             1795             1800
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     GAA AAC CTA TAA TCG TCG TAA AAA AAA ATA TGT TAC GTA AAA TTA CAA    3744
     Glu Asn Leu  *  Ser Ser  *  Lys Lys Ile Cys Tyr Val Lys Leu Gln
                 1805                 1810                     1815

5    ATG TAA AAA CAT AGT GTA AAA TGT ACA TAA AAT ACA TTT TTT GAC CTA    3792
     Met  *  Lys His Ser Val Lys Cys Thr  *  Asn Thr Phe Phe Asp Leu
                 1820             1825                     1830

     TAT TTT TTT TGT TAA TGC CAA ATT TTA TAC AGT AAA TCA ATA TGA ATG    3840
10   Tyr Phe Phe Cys  *  Cys Gln Ile Leu Tyr Ser Lys Ser Ile  *  Met
                 1835                 1840                 1845

     TAA CTA TTT GTA TTT CAA ATG TAA TTT ATT TAT GAA ATG GTC GTA AGA    3888
15    *  Leu Phe Val Phe Gln Met  *  Phe Ile Tyr Glu Met Val Val Arg
         1850                 1855                 1860

     TTA CCT CGG GTG AAG AAT AAC TTA TTC TGC ACC CTG GGT GAT GAA TAG    3936
     Leu Pro Arg Val Lys Asn Asn Leu Phe Cys Thr Leu Gly Asp Glu  *
     1865                 1870                 1875                 1880
20

     TAA CAC TAT ATA TAT ATA TAT ATA TAT ATA TAT ATA TAT ATA CCG GCT    3984
      *  His Tyr Ile Tyr Ile Tyr Ile Tyr Ile Tyr Ile Tyr Ile Pro Ala
                 1885                 1890                 1895

25   GCT GCT AAT GAT GTT AAT ATT TCG CAA GTA CCT AAG CTG GAT TTT TCT    4032
     Ala Ala Asn Asp Val Asn Ile Ser Gln Val Pro Lys Leu Asp Phe Ser
                 1900                 1905                 1910

     CCA TGA GAC ATC AAT CCA TAA TTG AAA TTG GTC ACG ACA GTT GAA TAG    4080
30   Pro  *  Asp Ile Asn Pro  *  Leu Lys Leu Val Thr Thr Val Glu  *
                 1915             1920                 1925

     TTG ATA GCT GAA AAT GAA ATC CAG CAT GCT ACT GTC TTG CCA TCT CCA    4128
     Leu Ile Ala Glu Asn Glu Ile Gln His Ala Thr Val Leu Pro Ser Pro
35       1930                 1935                 1940

     GAC TTG CTA ACA TGA ATT TTG TCT GCC TAC CTG TCA TTT GTA CCA ACG    4176
     Asp Leu Leu Thr  *  Ile Leu Ser Ala Tyr Leu Ser Phe Val Pro Thr
     1945                 1950                 1955                 1960
40

     TTC CCA ATT GCC CTC TCA TTA TTC GTG TGT ACC ATG CAT ATG TGT TTT    4224
     Phe Pro Ile Ala Leu Ser Leu Phe Val Cys Thr Met His Met Cys Phe
                 1965                 1970                 1975

45   AAC ATG ATT ATT GTT GGC TAT ATT TCT CTT TGG AAA CAT GAC TAA TTT    4272
     Asn Met Ile Ile Val Gly Tyr Ile Ser Leu Trp Lys His Asp  *  Phe
                 1980                 1985                 1990

     ATC ACC CGT TTT GTA TAA ACT GCT TGT TTT CAT ATC AGG ATG AAC TTT    4320
50   Ile Thr Arg Phe Val  *  Thr Ala Cys Phe His Ile Arg Met Asn Phe
                 1995             2000                 2005

     TGG GGA TAT TCT ACC ATA AAC TTC TTT TCA CCA ATG ACG AGA TAC ACA    4368
     Trp Gly Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr
55   2010                 2015                 2020

     TCA GGC GGG ATA AAA AAC TGT GGG CGT GAT GCC ATA AAT GAG TTC AAA    4416
     Ser Gly Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys
     2025                 2030                 2035                 2040
60

     ACT TTT GTA AGA GAG GCT CAC AAA CGG GGA ATT GAG GTA AGC AAG TCG    4464
     Thr Phe Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ser Lys Ser
                 2045                 2050                 2055
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    TAC GAG TTA GTT GCT CCT TTT GAA CTT ATC AAT TTG ATG CGA AGA CAT    4512
    Tyr Glu Leu Val Ala Pro Phe Glu Leu Ile Asn Leu Met Arg Arg His
                    2060            2065            2070
```

```
5   GTT ACT GCT AGG TGA TCC TGG ATG TTG TCT TCA ACC ATA CAG CTG AGG    4560
    Val Thr Ala Arg  *  Ser Trp Met Leu Ser Ser Thr Ile Gln Leu Arg
                    2075            2080            2085
```

```
    GTA ATG AGA ATG GTC CAA TAT TAT CAT TTA GGG GGG TCG ATA ATA CTA    4608
10  Val Met Arg Met Val Gln Tyr Tyr His Leu Gly Gly Ser Ile Ile Leu
                    2090            2095            2100
```

```
    CAT ACT ATA TGC TTG CAC CCA AGG TGA CAG ATC TTT CTT GCT GCG TAA    4656
    His Thr Ile Cys Leu His Pro Arg  *  Gln Ile Phe Leu Ala Ala  *
15  2105            2110            2115            2120
```

```
    TTG TTC TTT CAT AGA TGT ATA GAG CAT AGA TGT GTT ATG TAG TAG TTC    4704
    Leu Phe Phe His Arg Cys Ile Glu His Arg Cys Val Met  *   *  Phe
                    2125            2130            2135
20
```

```
    TTT TTC AAG GGG ATT ATG TTC ATG CAG GGA GAG TTT TAT AAC TAT TCT    4752
    Phe Phe Lys Gly Ile Met Phe Met Gln Gly Glu Phe Tyr Asn Tyr Ser
                    2140            2145            2150
```

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25  GGC TGT GGG AAT ACC TTC AAC TGT AAT CAT CCT GTG GTT CGT CAA TTC    4800
    Gly Cys Gly Asn Thr Phe Asn Cys Asn His Pro Val Val Arg Gln Phe
                    2155            2160            2165
```

```
    ATT GTA GAT TGT TTA AGG TAC AGA TAT ACA TTT TAC TTC TAG AAC TAC    4848
30  Ile Val Asp Cys Leu Arg Tyr Arg Tyr Thr Phe Tyr Phe  *  Asn Tyr
                    2170            2175            2180
```

```
    TTT TTC ATT TCT TTT GCT GCT TGT CAT TTT GAT ATG ATT AAT TTG CAA    4896
    Phe Phe Ile Ser Phe Ala Ala Cys His Phe Asp Met Ile Asn Leu Gln
35  2185            2190            2195            2200
```

```
    GCT TGT GGG GGT AAA TCT TTT GGT CAG CAT ATT GTA TCT TTA AAT GTC    4944
    Ala Cys Gly Gly Lys Ser Phe Gly Gln His Ile Val Ser Leu Asn Val
                    2205            2210            2215
40
```

```
    ACA AAT ACT AAT GTC CTG GTG CTT ATT GAT TTG GCA TCT TCA AAT TCT    4992
    Thr Asn Thr Asn Val Leu Val Leu Ile Asp Leu Ala Ser Ser Asn Ser
                    2220            2225            2230
```

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45  TCT CCA ATG AAA AGG GAA AAA TCT ACT GTA TGT CTC GTC AAC TAA TTT    5040
    Ser Pro Met Lys Arg Glu Lys Ser Thr Val Cys Leu Val Asn  *  Phe
                    2235            2240            2245
```

```
    ACT TTT GTT TTG CAG ATA CTG GGT GAT GGA AAT GCA TGT TGA TGG TTT    5088
50  Thr Phe Val Leu Gln Ile Leu Gly Asp Gly Asn Ala Cys  *  Trp Phe
                    2250            2255            2260
```

```
    TCG TTT TGA TCT TGC ATC CAT AAT GAC CAG AGG TTC CAG GTA ATT TGT    5136
    Ser Phe  *  Ser Cys Ile His Asn Asp Gln Arg Phe Gln Val Ile Cys
55  2265            2270            2275            2280
```

```
    ATT TAT TGT TTG TTT GCG TGT TGC CTT TTC AGA AGA TTC TTA AAA GAA    5184
    Ile Tyr Cys Leu Phe Ala Cys Cys Leu Phe Arg Arg Phe Leu Lys Glu
                    2285            2290            2295
60
```

```
    TGT TTC TTT TAC AAG TCT GTG GGA TCC AGT TAA CGT GTA TGG AGC TCC    5232
    Cys Phe Phe Tyr Lys Ser Val Gly Ser Ser  *  Arg Val Trp Ser Ser
                    2300            2305            2310
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     AAT AGA AGG TGA CAT GAT CAC AAC AGG GAC ACC TCT TGT TAC TCC ACC    5280
     Asn Arg Arg  *  His Asp His Asn Arg Asp Thr Ser Cys Tyr Ser Thr
             2315                 2320                 2325

  5  ACT TAT TGA CAT GAT CAG CAA TGA CCC AAT TCT TGG AGG CGT CAA GGT    5328
     Thr Tyr  *  His Asp Gln Gln  *  Pro Asn Ser Trp Arg Arg Gln Gly
             2330                 2335                 2340

     ACT TGT TTC ATC CAA CAC CTG TTG TCT GTG TGC ATT CAA TTG TTT TAA    5376
 10  Thr Cys Phe Ile Gln His Leu Leu Ser Val Cys Ile Gln Leu Phe  *
     2345                 2350                 2355             2360

     TAT GGT AAT GAT CAA TTT CCC AAT GTT GAT AAG GAA AAA AAA TGC AAG    5424
     Tyr Gly Asn Asp Gln Phe Pro Asn Val Asp Lys Glu Lys Lys Cys Lys
 15                  2365                 2370                 2375

     TAG CTC TCT TTA TCT GCT TCT TGT GAG TTA TGC TAA ACA TGT AGA TAC    5472
      *  Leu Ser Leu Ser Ala Ser Cys Glu Leu Cys  *  Thr Cys Arg Tyr
                 2380                 2385                 2390
 20

     TAC TAT ATT TCA ACT GTA TAT ACT TGA CAT ATT ATT GCT TCC TTG GGA    5520
     Tyr Tyr Ile Ser Thr Val Tyr Thr  *  His Ile Ile Ala Ser Leu Gly
                 2395                 2400                 2405

 25  GGC TCT CTT ATT CCT TTC CCC CGT TGC AAT TAT AGC TCA TTG CTG AAG    5568
     Gly Ser Leu Ile Pro Phe Pro Arg Cys Asn Tyr Ser Ser Leu Leu Lys
             2410                 2415                 2420

     CAT GGG ATG CAG GAG GCC TCT ATC AAG TAG GTC AAT TCC CTC ACT GGA    5616
 30  His Gly Met Gln Glu Ala Ser Ile Lys  *  Val Asn Ser Leu Thr Gly
     2425                 2430                 2435             2440

     ATG TTT GGT CTG AGT GGA ATG GGA AGG TAA GGT ACC TGT TAA AAG TTT    5664
     Met Phe Gly Leu Ser Gly Met Gly Arg  *  Gly Thr Cys  *  Lys Phe
 35  .            2445                 2450                 2455

     GAA TGG CAA ATA CTG ATA GAA ATA TAA CTT ATA TTT GCG ACA TAT ATA    5712
     Glu Trp Gln Ile Leu Ile Glu Ile  *  Leu Ile Phe Ala Thr Tyr Ile
                 2460                 2465                 2470
 40

     GAT AAA GCA AAA TAA TAC GCA TTC CAC CTG AAC TTT AAA GGG GCA CGC    5760
     Asp Lys Ala Lys  *  Tyr Ala Phe His Leu Asn Phe Lys Gly Ala Arg
                 2475                 2480                 2485

 45  AGA ATT ATC CCG CAT CTG TCT ACA AGA ATG ATA ACA CAT GTG CTG AAT    5808
     Arg Ile Ile Pro His Leu Ser Thr Arg Met Ile Thr His Val Leu Asn
     2490                 2495                 2500

     AGT GAA GTA CTA CTT CTC AAA TGT CTG AAT GAA CGC ACT AAC TCT TGT    5856
 50  Ser Glu Val Leu Leu Leu Lys Cys Leu Asn Glu Arg Thr Asn Ser Cys
     2505                 2510                 2515             2520

     GAG TGT CAA CCG AGC AAG AAA TAT TTG AGT TTT CTG CAA GAA ATT GTT    5904
     Glu Cys Gln Pro Ser Lys Lys Tyr Leu Ser Phe Leu Gln Glu Ile Val
 55                  2525                 2530                 2535

     CAT GTT GTG CTG TAT TAT ACT CCC TCC GTC CGA AAT TAT TTG TCG GAG    5952
     His Val Val Leu Tyr Tyr Thr Pro Ser Val Arg Asn Tyr Leu Ser Glu
                 2540                 2545                 2550
 60

     AAA TGG ATG TAT CTA GAC GTA TTT TAG TTC TAG ATA CAT CCA TTT TTA    6000
     Lys Trp Met Tyr Leu Asp Val Phe  *  Phe  *  Ile His Pro Phe Leu
                 2555                 2560                 2565
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      TCC ATT TCT GCA ACA AGT AGT TCC GGA CGG AGG GAG TAT CAT TTA ACA    6048
      Ser Ile Ser Ala Thr Ser Ser Ser Gly Arg Arg Glu Tyr His Leu Thr
      2570                2575                2580

 5    AAT ATA TGC ATG TTC GAA GTA AAT CCC CAC GAA TAA GCA TAT AAG ACG    6096
      Asn Ile Cys Met Phe Glu Val Asn Pro His Glu  *  Ala Tyr Lys Thr
      2585                2590                2595                2600

10    ATA TTG CTT TTT GAC TTG CAA CAC CTA AAC CTC ATT GTT TTC TCC TAG    6144
      Ile Leu Leu Phe Asp Leu Gln His Leu Asn Leu Ile Val Phe Ser  *
                          2605                2610                2615

      GAT TTT GGG TGT TCG AAG CAA GCA GCT GGT GAT ATT TAA TTT ACC TTT    6192
      Asp Phe Gly Cys Ser Lys Gln Ala Ala Gly Asp Ile  *  Phe Thr Phe
15                        2620                2625                2630

      GCC TTT ATT TGT AGC TTG ATT TGA GGG TGC GGC AAA GGT TTT AGC TTA    6240
      Ala Phe Ile Cys Ser Leu Ile  *  Gly Cys Gly Lys Gly Phe Ser Leu
                          2635                2640                2645
20
      GTA GTG TTT TGT AAA TTA TTA TAG TTT ATG TAT ATA CTC CTC ATT TGG    6288
      Val Val Phe Cys Lys Leu Leu  *  Phe Met Tyr Ile Leu Leu Ile Trp
                          2650                2655                2660

25    GCA CTT CCG TAC TGG TCC CAT AGA AGA TAA AAA TGG AAT GAT GTC TGG    6336
      Ala Leu Pro Tyr Trp Ser His Arg Arg  *  Lys Trp Asn Asp Val Trp
      2665                2670                2675                ·2680

30    CCA ATA ATT GTT GAC AAC ACT GTT GCG CAT TTG ATT TTT ATC AGG GAA    6384
      Pro Ile Ile Val Asp Asn Thr Val Ala His Leu Ile Phe Ile Arg Glu
                          2685                2690                2695

      TGG AAA ATT GAA ATC GGT AAG AAA CAT TGC GAT ATT AAG CTT GTA TAT    6432
      Trp Lys Ile Glu Ile Gly Lys Lys His Cys Asp Ile Lys Leu Val Tyr
35                        2700                2705                2710

      GCT AAT GCT GGT GGA TCT TTA AGA GGG AAC ATA TGA TCT CGT GTG CAT    6480
      Ala Asn Ala Gly Gly Ser Leu Arg Gly Asn Ile  *  Ser Arg Val His
                          2715                2720                2725
40
      CCA TCT TCA ACT AAA AAA ATA TGT TGC ACA TCT CCC ACG TCA CTT ACT    6528
      Pro Ser Ser Thr Lys Lys Ile Cys Cys Thr Ser Pro Thr Ser Leu Thr
                          2730                2735                2740

45    AGC TAT TTC ATC CAA GTA CTA ACT TGT GTG GTT GTC TCC TCA GTA CCG    6576
      Ser Tyr Phe Ile Gln Val Leu Thr Cys Val Val Val Ser Ser Val Pro
      2745                2750                2755                2760

50    GGA CAT TGT GCG CCA ATT CAT TAA AGG CAC TGA TGG ATT TGC TGG TGG    6624
      Gly His Cys Ala Pro Ile His  *  Arg His  *  Trp Ile Cys Trp Trp
                          2765                2770                2775

      TTT TGC CGA ATG TCT TTG TGG AAG TCC ACA CCT ATA CCA GGT AAG TTG    6672
      Phe Cys Arg Met Ser Leu Trp Lys Ser Thr Pro Ile Pro Gly Lys Leu
55                        2780                2785                2790

      TGG CAA TAC TTG GAA ATG GGT TGA GTG AAT GTC ACA TGG ATT TTT TAT    6720
      Trp Gln Tyr Leu Glu Met Gly  *  Val Asn Val Thr Trp Ile Phe Tyr
                          2795.               2800                2805
60
      ATA TAC CAC ATG ATG ATA CAC ATG TAA ATA TAT AAC GAT TAT AGT GTA    6768
      Ile Tyr His Met Met Ile His Met  *  Ile Tyr Asn Asp Tyr Ser Val
                          2810                2815                2820
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     TGC ATA TGC ATT TGG CTA AGA AGT ACT CCC TCC CTT AGT AAA AGT TAG    6816
     Cys Ile Cys Ile Trp Leu Arg Ser Thr Pro Ser Leu Ser Lys Ser  *
     2825              2830              2835              2840

 5   TAC AAA GTT GAG TCA TCT ATT TTG GAA CGG AGG GAG TAT AAG TGT ATA    6864
     Tyr Lys Val Glu Ser Ser Ile Leu Glu Arg Arg Glu Tyr Lys Cys Ile
              2845              2850              2855

     CAC TAG TGC AAT ATA TAG GTT TTA ACA CCC AAC TTG CCA ATG AAG GAA    6912
10   His  *  Cys Asn Ile  *  Val Leu Thr Pro Asn Leu Pro Met Lys Glu
              2860              2865              2870

     CAT AGG GCT TTC TAG TTA TCT TAT TTA TTT GTC TGG TGA ATA ATC CAC    6960
     His Arg Ala Phe  *  Leu Ser Tyr Leu Phe Val Trp  *  Ile Ile His
15            2875              2880              2885

     TGA AAA ATT CCA GCC ATG TCA TTT TTT AGG GGG GGA GAA GAA ACT ACA    7008
      *  Lys Ile Pro Ala Met Ser Phe Phe Arg Gly Gly Glu Glu Thr Thr
              2890              2895              2900
20

     TTG ATT TTT CCC CCT AAA AAA AGC CAT CTC AGA TTT CAT AGG TAA CTT    7056
     Leu Ile Phe Pro Pro Lys Lys Ser His Leu Arg Phe His Arg  *  Leu
     2905              2910              2915              2920

25   GCT TTT CTG TAA AGA AAT GAA AAC GAC TTC ATA CTT TCT GTC GAT TAT    7104
     Ala Phe Leu  *  Arg Asn Glu Asn Asp Phe Ile Leu Ser Val Asp Tyr
                  2925              2930              2935

     AAG TGT ATA CAC TAG TGC AAT ATA TAG GTT TTA ACA CCC AAC TTG CCA    7152
30   Lys Cys Ile His  *  Cys Asn Ile  *  Val Leu Thr Pro Asn Leu Pro
              2940              2945              2950

     ATG AAG GAA CAT AGG GCT TTC TAG TTA TCT TAT TTA TTT GCT GGT GAA    7200
     Met Lys Glu His Arg Ala Phe  *  Leu Ser Tyr Leu Phe Ala Gly Glu
35            2955              2960              2965

     TAA TCC ACT GAA AAA TTC CAG CCA TGT CAT TTT TTA GGG GGG AGA AGA    7248
      *  Ser Thr Glu Lys Phe Gln Pro Cys His Phe Leu Gly Gly Arg Arg
              2970              2975              2980
40

     AAC TAT ATT GAT TTT TCC CCC TAA AAA AAG CCA TCT CAG ATT CAT AGG    7296
     Asn Tyr Ile Asp Phe Ser Pro  *  Lys Lys Pro Ser Gln Ile His Arg
     2985              2990              2995              3000

45   AAC TTG CTT TTC TGT AAA GAA ATG AAA ACG ACT TCA TAC TTT CTG CGG    7344
     Asn Leu Leu Phe Cys Lys Glu Met Lys Thr Thr Ser Tyr Phe Leu Arg
                  3005              3010              3015

     CGC TTA CTT AGC TCG ATG GAT ATT TGT AAG ATG AAT GCC AAA TTA TTT    7392
50   Arg Leu Leu Ser Ser Met Asp Ile Cys Lys Met Asn Ala Lys Leu Phe
              3020              3025              3030

     GGC GGG ATT TGA TCG TTA TTC CAA ATT TCA TTT GGT TTC TCT AGC AAT    7440
     Gly Gly Ile  *  Ser Leu Phe Gln Ile Ser Phe Gly Phe Ser Ser Asn
55            3035              3040              3045

     CAA CCC AGT ACC TTG TTA TTG GCA CTG CAA TTT CTT ATT GAT TAA TCA    7488
     Gln Pro Ser Thr Leu Leu Leu Ala Leu Gln Phe Leu Ile Asp  *  Ser
              3050              3055              3060
60

     GGC AGG AGG AAG GAA ACC TTG GCA CAG TAT CAA CTT GGT ATG TGC ACA    7536
     Gly Arg Arg Lys Glu Thr Leu Ala Gln Tyr Gln Leu Gly Met Cys Thr
     3065              3070              3075              3080
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    TGA TGG ATT TAC ACT GGG TGA TTT GGT ACA TAT AAT ACC AAG TCA ATT    7584
     *  Trp Ile Tyr Thr Gly  *  Phe Gly Thr Tyr Asn Thr Lys Ser Ile
                        3085              3090                3095

 5  TAC CAA ATG GGG AGA CCA ATA GAG ATG GAG AAA ATC ACA ATC TTA GCT    7632
    Tyr Gln Met Gly Arg Pro Ile Glu Met Glu Lys Ile Thr Ile Leu Ala
                 3100              3105               3110

    GGA ATT GTG GGG AGG TAA TTC TGA ACT CTC CTT TTT TTT TGA AAT TTT    7680
10  Gly Ile Val Gly Arg  *  Phe  *  Thr Leu Leu Phe Phe  *  Asn Phe
                 3115              3120              3125

    CAT GCT TTA CAT AAT AGT CAA ATG GCT GAC AAA TGT CGT TGT ATG GTT    7728
    His Ala Leu His Asn Ser Gln Met Ala Asp Lys Cys Arg Cys Met Val
15           3130              3135              3140

    CTC TCT ACC TAA ACC GTT AAG GCA GTA AGA GTT TCC CTA CAA GAT CTC    7776
    Leu Ser Thr  *  Thr Val Lys Ala Val Arg Val Ser Leu Gln Asp Leu
    3145              3150               3155               3160
20
    TTT GTT CGT ATA ATT GTA TTT TCT AGA GAA AAG TTG CCT TCA ATT TTG    7824
    Phe Val Arg Ile Ile Val Phe Ser Arg Glu Lys Leu Pro Ser Ile Leu
                 3165              3170               3175

25  TGC ACG CGG CAG TAC AGG AAT TGT GGT TAT AAA TAT TGA TAC AGG CTG    7872
    Cys Thr Arg Gln Tyr Arg Asn Cys Gly Tyr Lys Tyr  *  Tyr Arg Leu
                 3180              3185              3190

    ACC ATC GTT ACT AAT AGG GGG AAC AAT AAG CAC ATT TTT TTA ATA GCA    7920
30  Thr Ile Val Thr Asn Arg Gly Asn Asn Lys His Ile Phe Leu Ile Ala
                 3195              3200              3205

    AAG GCA TCA CCC TTG TTC CGT TTC CAA TGA AAT CAC AGT ATC CGA ACC    7968
    Lys Ala Ser Pro Leu Phe Arg Phe Gln  *  Asn His Ser Ile Arg Thr
35           3210              3215              3220

    ATA AGT TTT ACA AGT ATG CGT AGA GAG AAA TAA AGT ATC AAC CCG GCA    8016
    Ile Ser Phe Thr Ser Met Arg Arg Glu Lys  *  Ser Ile Asn Pro Ala
    3225              3230              3235               3240
40
    GAA ACA GTT GTT TCA GGC GCA AAG AGA AAA GGA AAC GAT ATG CTC TAT    8064
    Glu Thr Val Val Ser Gly Ala Lys Arg Lys Gly Asn Asp Met Leu Tyr
                 3245              3250               3255

45  TAC ATC AAC CTT TTA GCA TTT AGG GAC GAC CAG CAT CAT CCC ATC TTC    8112
    Tyr Ile Asn Leu Leu Ala Phe Arg Asp Asp Gln His His Pro Ile Phe
                 3260              3265              3270

    AAT CAA CTG GAG CGA GGT CAC CTC CAA TCT TCT CAG CAG CCT CAG AGT    8160
50  Asn Gln Leu Glu Arg Gly His Leu Gln Ser Ser Gln Gln Pro Gln Ser
                 3275              3280              3285

    GGT GAC CTC CCA AGC AAG TGC ATC AGC ATC CAT CAT CTG GGG GTT GGG    8208
    Gly Asp Leu Pro Ser Lys Cys Ile Ser Ile His His Leu Gly Val Gly
55           3290              3295              3300

    CAC ATA CCA TGA GCA CAA TCA CCT GAA TTT GAT GAA TTT TCC TCT GTT    8256
    His Ile Pro  *  Ala Gln Ser Pro Glu Phe Asp Glu Phe Ser Ser Val
    3305              3310              3315               3320
60
    TAC CTT GCA GCA GAC CCC TGC CGT ATA AAT GGT TTT AAA TGA CAG CAT    8304
    Tyr Leu Ala Ala Asp Pro Cys Arg Ile Asn Gly Phe Lys  *  Gln His
                 3325              3330              3335
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      GTT CTT TCA GTT TGA GCA AAA TTT GTG CAA TTG CAA AGA AGC TTT AGA    8352
      Val Leu Ser Val  *  Ala Lys Phe Val Gln Leu Gln Arg Ser Phe Arg
                 3340                  3345                  3350

 5    ATC ATG TGG AAC ATG CAC TTA CAT TTC ATC TGA CAA TAT AGG AAG GAG    8400
      Ile Met Trp Asn Met His Leu His Phe Ile  *  Gln Tyr Arg Lys Glu
                 3355                  3360                  3365

10    AGC CCG ACG TCG CAT GCT CCT CTA GAC TCG AGG AAT TCG CAA GAT TGT    8448
      Ser Pro Thr Ser His Ala Pro Leu Asp Ser Arg Asn Ser Gln Asp Cys
                 3370                  3375                  3380

      CTG TCA AAA GAT TGA GGA AGA GGC AGA TGC GCA ATT TCT TTG TTT GTC    8496
15    Leu Ser Lys Asp  *  Gly Arg Gly Arg Cys Ala Ile Ser Leu Phe Val
      3385                  3390                  3395              3400

      TCA TGG TTT CTC AAG TAA GAC TTA TAT CTG ATC TCT TCA ATT TTT GAG    8544
      Ser Trp Phe Leu Lys  *  Asp Leu Tyr Leu Ile Ser Ser Ile Phe Glu
                 3405                  3410                  3415
20
      ATT GCC TGT TTT TCA CAA TGG CAT ATG TTG TCA GGT GAA ACA TCC AAT    8592
      Ile Ala Cys Phe Ser Gln Trp His Met Leu Ser Gly Glu Thr Ser Asn
                 3420                  3425                  3430

25    CCC AGT ATT AAT AGA GCC AAC ATG AAG GGA TTG CTT ATC TGA GAT ATC    8640
      Pro Ser Ile Asn Arg Ala Asn Met Lys Gly Leu Leu Ile  *  Asp Ile
                 3435                  3440                  3445

      TGC CAA AGT TGA ATT CTT AGA TTC ACC TTC TTC AGT ATT TCA GAC CTT    8688
30    Cys Gln Ser  *  Ile Leu Arg Phe Thr Phe Phe Ser Ile Ser Asp Leu
                 3450                  3455                  3460

      CTA AGC ATT TTC ATT TTT TTT TTC AAT TGT TAG GGA GTT CCA ATG TTT    8736
35    Leu Ser Ile Phe Ile Phe Phe Phe Asn Cys  *  Gly Val Pro Met Phe
      3465                  3470                  3475              3480

      TAC ATG GGC GAT GAA TAT GGC CAC ACA AAA GGG GGC AAC AAC AAT ACA    8784
      Tyr Met Gly Asp Glu Tyr Gly His Thr Lys Gly Gly Asn Asn Asn Thr
                 3485                  3490                  3495
40
      TAC TGC CAT GAT TCT TAT GTC AGT ACA ATT TGG TCA CAT ATT GTT GTT    8832
      Tyr Cys His Asp Ser Tyr Val Ser Thr Ile Trp Ser His Ile Val Val
                 3500                  3505                  3510

45    CTA AGT AAC TAT CTT CAA ATC TTT GCA TTC ATC CGT CAT GGC TCT TCT    8880
      Leu Ser Asn Tyr Leu Gln Ile Phe Ala Phe Ile Arg His Gly Ser Ser
                 3515                  3520                  3525

      GTA GGT CAA TTA TTT TCG CTG GGA TAA AAA AGA ACA ATA CTC TGA CTT    8928
50    Val Gly Gln Leu Phe Ser Leu Gly  *  Lys Arg Thr Ile Leu  *  Leu
                 3530                  3535                  3540

      GCA AAG ATT CTG CTG CCT CAT GAC CAA ATT CCG CAA GTA AGT ATT CCG    8976
55    Ala Lys Ile Leu Leu Pro His Asp Gln Ile Pro Gln Val Ser Ile Pro
      3545                  3550                  3555              3560

      TTG AAT AAT TTC TGT GTA GAA CCA CTG AAG GTG CCT CCA AAC GCT AAG    9024
      Leu Asn Asn Phe Cys Val Glu Pro Leu Lys Val Pro Pro Asn Ala Lys
                 3565                  3570                  3575
60
      CGA GCA AGG TCA ATT TCA CAC CCT AAT CAA GTT GGT GTT GTC TAT TTG    9072
      Arg Ala Arg Ser Ile Ser His Pro Asn Gln Val Gly Val Val Tyr Leu
                 3580                  3585                  3590
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     TGT ATT TGA TCT GCT GCA CTG TAG GGA GTG CGA GGG TCT TGG CCT TGA    9120
     Cys Ile  *  Ser Ala Ala Leu  *  Gly Val Arg Gly Ser Trp Pro  *
             3595                 3600                 3605

  5  GGA CTT TCC AAC GGC CGA ACG GCT GCA GTG GCA TGG TCA TCA GCC TGG    9168
     Gly Leu Ser Asn Gly Arg Thr Ala Ala Val Ala Trp Ser Ser Ala Trp
             3610             3615                 3620

     GAA GCC TGA TTG GTC TGA GAA TAG CCG ATT CGT TGC CTT TTC CAT GGT    9216
 10  Glu Ala  *  Leu Val  *  Glu  *  Pro Ile Arg Cys Leu Phe His Gly
     3625                 3630                 3635                 3640

     ACA CAT ATA GTT CTG ACA CTT CAC TAT AGT TGT TTT AAA AAA GAA AAT    9264
     Thr His Ile Val Leu Thr Leu His Tyr Ser Cys Phe Lys Lys Glu Asn
 15              3645                 3650                 3655

     TTA ACT CAA AAG TAA ATT ATG GAG  A                                9289
     Leu Thr Gln Lys  *  Ile Met Glu
             3660
 20
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